

ALIGNMENTS

RESULT 1

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US-09-985-689A-1
; Sequence 1, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483U80
; CURRENT APPLICATION NUMBER: US/09/985.689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-1
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Query Match      100.0%; Score 2247; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.9e-176;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NDVARGIVKADVAGSSYGLYGQGI VAVADTGLDTGRNDSSMHFAFRKII TALTALVALGRTN 60
Db      1 NDVARGIVKADVAGSSYGLYGQGI VAVADTGLDTGRNDSSMHFAFRKII TALTALVALGRTN 60

Qy      61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db      61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120

Qy      121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNCGGTISAPGTAKNAI 180
Db      121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNCGGTISAPGTAKNAI 180

Qy      181 TVGATENLRPSFGSYADININHAQFSSRGPTKDGRIKPDVMA PGTFILSARSSSLAPDSSF 240
Db      181 TVGATENLRPSFGSYADININHAQFSSRGPTKDGRIKPDVMA PGTFILSARSSSLAPDSSF 240

Qy      241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 300
Db      241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 300

Qy      301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPLKISLWMSDAPASTTA 360
Db      301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPLKISLWMSDAPASTTA 360

Qy      361 SVTLVNDLDELVTAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420
Db      361 SVTLVNDLDELVTAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420

Qy      421 VPVGPQTFTSLAIVN 434
Db      421 VPVGPQTFTSLAIVN 434
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RESULT 2

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US-09-509-814A-6
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; Sequence 6, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUMI
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/509.814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JF98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-6
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Query Match      100.0%; Score 2247; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.2e-175;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NDVARGIVKADVAGSSYGLYGQGI VAVADTGLDTGRNDSSMHFAFRKII TALTALVALGRTN 60
Db      207 NDVARGIVKADVAGSSYGLYGQGI VAVADTGLDTGRNDSSMHFAFRKII TALTALVALGRTN 266

Qy      61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db      267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 326

Qy      121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNCGGTISAPGTAKNAI 180
Db      327 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNCGGTISAPGTAKNAI 386

Qy      181 TVGATENLRPSFGSYADININHAQFSSRGPTKDGRIKPDVMA PGTFILSARSSSLAPDSSF 240
Db      387 TVGATENLRPSFGSYADININHAQFSSRGPTKDGRIKPDVMA PGTFILSARSSSLAPDSSF 446

Qy      241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 300
Db      447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 506

Qy      301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPLKISLWMSDAPASTTA 360
Db      507 PNGNQGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPLKISLWMSDAPASTTA 566

Qy      361 SVTLVNDLDELVTAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420
Db      567 SVTLVNDLDELVTAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 626

Qy      421 VPVGPQTFTSLAIVN 434
Db      627 VPVGPQTFTSLAIVN 640
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RESULT 3

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US-09-920-954-6
; Sequence 6, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
```

; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-6

Query Match 100.0%; Score 2247; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.2e-175;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 266

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHNSWGAANGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
Db 327 AGARIHNSWGAANGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPTFILSARSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPTFILSARSSLAPDSSF 446

Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAAIAGAADIGLGY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAAIAGAADIGLGY 506

Qy 301 PNGNQGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNQGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 566

Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 626

Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

RESULT 4
US-09-509-814A-8
; Sequence 8, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE

; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-8

Query Match 99.8%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 3e-175;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 266

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHNSWGAANGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
Db 327 AGARIHNSWGAANGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPTFILSARSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPTFILSARSSLAPDSSF 446

Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAAIAGAADIGLGY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAAIAGAADIGLGY 506

Qy 301 PNGNQGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNQGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 566

Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 626

Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

RESULT 5
US-09-920-954-8
; Sequence 8, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07

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; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-8

Query Match          99.8%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 3e-175;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 266

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 446

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVKNRGITPKPSLLKALIAAGADIIGLY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVKNRGITPKPSLLKALIAAGADIIGLY 506

Qy 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLDLVITAPNGTYVGNDFTPSYNDWGRNNVENVFVINAPOSQGYTTIEVOAYN 420
Db 567 SVTLVNDLDLVITAPNGTYVGNDFTPSYNDWGRNNVENVFVINAPOSQGYTTIEVOAYN 626

Qy 421 VPVGQPTFSLAIVN 434
Db 627 VPVGQPTFSLAIVN 640

RESULT 6
US-09-985-689A-2
; Sequence 2, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/09/985,689A
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-2

Query Match          97.2%; Score 2183; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 2.1e-170;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

; ORGANISM: Bacillus sp.
US-09-985-689A-2

Query Match          97.5%; Score 2191; DB 2; Length 434;
Best Local Similarity 96.5%; Pred. No. 2.7e-171;
Matches 419; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

Qy 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 240

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVKNRGITPKPSLLKALIAAGADIIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVKNRGITPKPSLLKALIAAGADIIGLY 300

Qy 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360

Qy 361 SVTLVNDLDLVITAPNGTYVGNDFTPSYNDWGRNNVENVFVINAPOSQGYTTIEVOAYN 420
Db 361 SVTLVNDLDLVITAPNGTYVGNDFTPSYNDWGRNNVENVFVINAPOSQGYTTIEVOAYN 420

Qy 421 VPVGQPTFSLAIVN 434
Db 421 VPVGQPTFSLAIVN 434

RESULT 7
US-09-509-814A-4
; Sequence 4, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-4

Query Match          97.2%; Score 2183; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 2.1e-170;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;
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Qy	1	NDVARGIVKADVAQSSYGLYGQGGQIVAVADTGLDGTGRNDSMHEAFRGKITALLYALGRTN	60
Db	206	NDVARGIVKADVAQSSYGLYGQGGQIVAVADTGLDGTGRNDSMHEAFRGKITALLYALGRTN	265
Qy	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAFS	120
Db	266	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAFS	325
Qy	121	AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI	180
Db	326	AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI	385
Qy	181	TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSLAPDSSF	240
Db	386	TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSLAPDSSF	445
Qy	241	WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALTAGAADIGLY	300
Db	446	WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALTAGAADIGLY	505
Qy	301	PNGNQGWGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA	360
Db	506	PNGNQGWGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA	565
Qy	361	SVTLVNDLVLITAPNGTQYVGNDFTSPYNDNWDGRNNVFNAPQSGTYYTIEVOAYN	420
Db	566	SVTLVNDLVLITAPNGTRYVGNDFSAFPDNNWDGRNNVFNAPQSGTYYTIEVOAYN	625
Qy	421	VPVGPQTFSLAIVN	434
Db	626	VPVGPQNFSLAIVN	639
RESULT 8			
US-09-920-954-4			
; Sequence 4, Application US/09920954			
; Patent No. 6759228			
; GENERAL INFORMATION:			
; APPLICANT: TAKAIWA, MIKIO			
; APPLICANT: OKUDA, MITSUYOSHI			
; APPLICANT: SAEKI, KATSUHIISA			
; APPLICANT: KUBOTA, HIROMI			
; APPLICANT: HITOMI, JUN			
; APPLICANT: KAGEYAMA, YASUSHI			
; APPLICANT: SHIKATA, SHITSUM			
; APPLICANT: NOMURA, MASAFUMI			
; TITLE OF INVENTION: ALKALINE PROTEASE			
; FILE REFERENCE: 0327-0832-0PCT			
; CURRENT APPLICATION NUMBER: US/09/920,954			
; CURRENT FILING DATE: 2001-08-03			
; PRIOR APPLICATION NUMBER: 09/509,814			
; PRIOR FILING DATE: 2000-04-06			
; PRIOR APPLICATION NUMBER: PCT/JP98/04528			
; PRIOR FILING DATE: 1998-10-07			
; PRIOR APPLICATION NUMBER: JP 9-274570			
; PRIOR FILING DATE: 1997-06-08			
; NUMBER OF SEQ ID NOS: 24			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 4			
; LENGTH: 639			
; TYPE: PRT			
; ORGANISM: Bacillus sp.			
US-09-920-954-4			
Query Match 97.2%; Score 2183; DB 2; Length 639;			
Best Local Similarity 96.3%; Pred. No. 2.1e-170;			
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;			
Qy	1	NDVARGIVKADVAQSSYGLYGQGGQIVAVADTGLDGTGRNDSMHEAFRGKITALLYALGRTN	60
Db	206	NDVARGIVKADVAQSSYGLYGQGGQIVAVADTGLDGTGRNDSMHEAFRGKITALLYALGRTN	265
Qy	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAFS	120

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (70)..(70)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (74)..(74)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (89)..(89)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (102)..(102)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
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OTHER INFORMATION: Xaa is any amino acid

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OTHER INFORMATION: Xaa is any amino acid
US-09-509-814A-1

Query Match 95.9%; Score 2155; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 4.1e-168;
Matches 418; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAPRGKITALVALGRTN 60
Db 206 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAPRGKITALVALGRTN 265
Qy 61 NANDTNGHGHVAGSVLGNSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 266 NANDTNGHGHVAGSVLGNSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 325
Qy 121 AGARIHTNSWCAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 326 AGARIHTNSWCAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 385
Qy 181 TVGATENLRPSFGSYADNINHVAFSSRGPTKDRIKPDVMPAGTFFILSARSSLPDSSSF 240
Db 386 TVGATENLRPSFGSYADNINHVAFSSRGPTKDRIKPDVMPAGTFFILSARSSLPDSSSF 445
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAALIAAGADIGLY 300
Db 446 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAALIAAGADIGLY 505
Qy 301 PNGNQGWGRVTLDKSLNVAYYNNESSLSTSKATYSFTATAGKPKISLVMSDAPASTTA 360
Db 506 PNGNQGWGRVTLDKSLNVAYYNNESSLSTSKATYSFTATAGKPKISLVMSDAPASTTA 565
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFNAPQSGTYYTIEVQAYN 420
Db 566 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFNAPQSGTYYTIEVQAYN 625
Qy 421 VPVGQTFSLAIVN 434
Db 626 VPVGQTFSLAIVN 639

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RESULT 10
US-09-920-954-1
; Sequence 1, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Bacillus sp.
; FEATURE:
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; LOCATION: (23)..(23)
; OTHER INFORMATION: Xaa is any amino acid
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; NAME/KEY: misc feature
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; OTHER INFORMATION: Xaa is any amino acid
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; LOCATION: (632)..(632)
; OTHER INFORMATION: Xaa is any amino acid
US-09-920-954-1

Query Match 95.9%; Score 2155; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 4.1e-168;
Matches 418; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVQSSVGLYGQGOIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
Db 206 NDVARGIVKADVQSSVGLYGQGOIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 265

QY 61 NANDTNGHGTTHVAGSVLNGSTNGKGMAPQANLVFQSIMDSGGGLGGLPSNLTTLFSQAYS 120
Db 266 NANDTNGHGTTHVAGSVLNGSTNGKGMAPQANLVFQSIMDSGGGLGGLPSNLTTLFSQAYS 325

QY 121 AGARIHTNSGAAVNGAYTTDSRNVDVVRKNDMTILFAAGNEGPNGTISAPGTAKNAI 180
Db 326 AGARIHTNSGAAVNGAYTTDSRNVDVVRKNDMTILFAAGNEGPNGTISAPGTAKNAI 385

QY 181 TVGATENLRPFSGVADNINHVAFSSRGPTKDGRIKPDVMAPGTIFLSARSSILAPDSSF 240
Db 386 TVGATENLRPFSGVADNINHVAFSSRGPTKDGRIKPDVMAPGTIFLSARSSILAPDSSF 445

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 446 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 505

QY 301 PNGNGQWRVTLDKSLNVAYNNESSLSQKATYFTATAGKPKLSIIVMSDAPASTTA 360
Db 506 PNGNGQWRVTLDKSLNVAYNNESSLSQKATYFTATAGKPKLSIIVMSDAPASTTA 565

QY 361 SVTLVNDLVLVTAPNGTYGVNDFTSPVNDMDGNNVNFVINAPOSQGTITIEVQAYN 420
Db 566 SVTLVNDLVLVTAPNGTYGVNDFTSPVNDMDGNNVNFVINAPOSQGTITIEVQAYN 625

QY 421 VPVGPQTTFSLAVN 434
Db 626 VPVGPQXFSLAVN 639

RESULT 11
US-09-509-814A-2
; Sequence 2, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUO
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OpCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 640
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; ORGANISM: Bacillus sp.
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, LOCATION: (325)..(325)
, OTHER INFORMATION: Xaa is any amino acid
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, OTHER INFORMATION: Xaa is any amino acid
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, NAME/KEY: misc feature
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, OTHER INFORMATION: Xaa is any amino acid
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, US-09-920-954-2

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2

Db 567 SVTLVNDLVLVITAPNGTXYVGNDFXXPXXNMDGRNNVENVFINXPSQSGTYYTIEVQAYN 626

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Db 627 VPVGPQXFSLAIVN 640

RESULT 13
US-09-985-689A-6
; Sequence 6, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-6

Query Match 95.4%; Score 2143; DB 2; Length 434;
Best Local Similarity 93.5%; Pred. No. 2.3e-167;
Matches 406; Conservative 19; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVQAQSSYGLYGQGVIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
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Db 1 NDVARGIVKADVQAQSSYGLYGQGVIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
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Qy 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSOAYS 120
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Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
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Db 121 AGARIHTNSWGAAPVNGAYTTDSRNVDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI 180
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Qy 181 TVGATENLRSPFGSYADNINHVAQFSSRGPTKGRIKPDVMAPGTFTLSARSSLAPDSSF 240
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Db 181 TVGATENLRSPFGSYADNINHVAQFSSRGPTKGRIKPDVMAPGTFTLSARSSLAPDSSF 240
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Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALTAGADIGLGY 300
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Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALTAGADIGLGY 300
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Qy 301 PNGNQGWGRVTLDKSLNVAAYNNESSLSSTSQKATYSFTATAGPKLKLISLWSDAPASTTA 360
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Db 301 PNGNQGWGRVTLDKSLNVAAYNNESSLSSTNQKATYSFTAQSGKPLKLSLWSDAPASTSA 360
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Qy 361 SVTLVNDLVLVITAPNGTQVGNDFTPSYNDNDGRNNVENVFINAPQSGTYYTIEVQAYN 420
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Db 361 SVTLVNDLVLVITAPNGTKYVGNDFTPAPYDNNMDGRNNVENVFINAPQSGTYYTIEVQAYN 420
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Qy 421 VPVGPQTFSLAIYN 434
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Db 421 VPOGPQAFSLAIYN 434
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RESULT 14
US-09-985-689A-7
; Sequence 7, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-7

Query Match 94.6%; Score 2125.5; DB 2; Length 433;
Best Local Similarity 93.5%; Pred. No. 6.2e-166;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NDVARGIVKADVQAQSSYGLYGQGVIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
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Db 1 NDVARGIVKADVQAQNNFGLYGQGVIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
|||

Qy 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSOAYS 120
|||

Db 61 NANDPNGHGHVAGSVLGN-ATNKGMAPOANLVFQSIMDSGGGLGGLPANLQTLFSOAYS 119
|||

Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
|||

Db 120 AGARIHTNSWGAAPVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 179
|||

Qy 181 TVGATENLRSPFGSYADNINHVAQFSSRGPTKGRIKPDVMAPGTFTLSARSSLAPDSSF 240
|||

Db 180 TVGATENLRSPFGSYADNINHVAQFSSRGPTKGRIKPDVMAPGTFTLSARSSLAPDSSF 239
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Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALTAGADIGLGY 300
|||

Db 240 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAAALTAGADVGLGF 299
|||

Qy 301 PNGNQGWGRVTLDKSLNVAAYNNESSLSSTSQKATYSFTATAGPKLKLISLWSDAPASTTA 360
|||

Db 300 PNGNQGWGRVTLDKSLNVAAYNNESSLSSTSQKATYSFTAQAGKPLKISLWSDAPGSTTA 359
|||

Qy 361 SVTLVNDLVLVITAPNGTQVGNDFTPSYNDNDGRNNVENVFINAPQSGTYYTIEVQAYN 420
|||

Db 360 SVTLVNDLVLVITAPNGTKYVGNDFTPAPYDNNMDGRNNVENVFINAPQSGTYYTIEVQAYN 419
|||

Qy 421 VPVGPQTFSLAIYN 434
|||||

Db 420 VPVSPQTFSLAIYH 433
|||||

RESULT 15
US-08-873-479-42
; Sequence 42, Application US/08873479
; Patent No. 5891701
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan
; APPLICANT: Lynne, Christianson

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 30, 2006, 08:34:11 ; Search time 166 Seconds
(without alignments)
1092.397 Million cell u

Title: US-10-820-712A-1

Perfect score:

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAYNVPVGPQTFSLAIVN 434

Scoring table: BLOSUM62

Scoring cubic: 2500002
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs. 417829326 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length:	200000000
Maximum DB seq length:	200000000

Post-processing: Minimum Match 0%

100% processing: Minimum Match 0%
Maximum Match 100%

Database :

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Database : Published Applications_AA_Main.*
1: /cn2_6/prodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cn2_6/prodata/1/pubpaa/US08_PUBCOMB.pcp.*
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4: /cn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pcp.*
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6: /cn2_6/prodata/1/pubpaa/US11_PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
					ID	Description
1	2247	100.0	434	3	US-09-985-689A-1	Sequence 1, Appli
2	2247	100.0	434	2	US-10-385-662-2	Sequence 2, Appli
3	2247	100.0	434	4	US-10-456-479-2	Sequence 2, Appli
4	2247	100.0	434	4	US-10-837-566-1	Sequence 2, Appli
5	2247	100.0	434	5	US-10-820-712A-1	Sequence 1, Appli
6	2247	100.0	434	5	US-10-820-714A-1	Sequence 1, Appli
7	2247	100.0	640	3	US-09-920-954-6	Sequence 6, Appli
8	2247	100.0	640	4	US-10-456-479-4	Sequence 4, Appli
9	2247	100.0	640	4	US-10-784-870-6	Sequence 6, Appli
10	2247	100.0	640	5	US-10-820-712A-3	Sequence 3, Appli
11	2247	100.0	640	5	US-10-820-714A-3	Sequence 3, Appli
12	2242	99.8	434	4	US-10-456-479-11	Sequence 11, Appl
13	2242	99.8	434	5	US-10-820-712A-14	Sequence 14, Appl
14	2242	99.8	434	5	US-10-820-714A-15	Sequence 15, Appl
15	2242	99.8	640	3	US-09-920-954-8	Sequence 8, Appli
16	2242	99.8	640	4	US-10-784-870-8	Sequence 8, Appli
17	2191	97.5	434	3	US-09-985-689A-2	Sequence 2, Appli
18	2191	97.5	434	4	US-10-456-479-10	Sequence 10, Appl
19	2191	97.5	434	4	US-10-837-566-2	Sequence 2, Appli
20	2191	97.5	434	5	US-10-820-712A-12	Sequence 12, Appl
21	2191	97.5	434	5	US-10-820-714A-13	Sequence 13, Appl
22	2183	97.2	639	4	US-09-920-954-4	Sequence 4, Appli
23	2183	97.2	639	4	US-10-784-870-4	Sequence 4, Appli
24	2155	95.9	639	3	US-09-920-954-1	Sequence 1, Appli
25	2155	95.9	639	4	US-10-784-870-1	Sequence 1, Appli
26	2155	95.9	640	3	US-09-920-954-2	Sequence 2, Appli
27	2155	95.9	640	4	US-10-784-870-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-985-689A-1

; Sequence 1, Application US/09985689A
; Publication No. US20030022351A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-1

Query Match 100.0%; Score 2247; DB 3; Length 434;

Best Local Similarity 100.0%; Pred. No. 3.6e-171;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	NDVARGIVKADVAGSSYGLYGQGI	VADVADTGLD	GRNDSSMH	EAFRGKIT	ALYALGR	TN 60
DB	1	NDVARGIVKADVAGSSYGLYGQGI	VADVADTGLD	GRNDSSMH	EAFRGKIT	ALYALGR	TN 60
QY	61	NANDTNGHGT	HVAGSVLNGST	TKGMAPOANL	VFQSI	MDSGGGLG	PSNLQTLFSQAYS 120
DB	61	NANDTNGHGT	HVAGSVLNGST	TKGMAPOANL	VFQSI	MDSGGGLG	PSNLQTLFSQAYS 120
QY	121	AGARIHTNSGAA	VNGAYTTDS	RNVDDYVR	KNDMTIL	FAAGNEGP	NGGTISAPGTAKNAI 180
DB	121	AGARIHTNSGAA	VNGAYTTDS	RNVDDYVR	KNDMTIL	FAAGNEGP	NGGTISAPGTAKNAI 180
QY	181	TVGATENLR	PSFGSYADN	INHVAQF	SSRGPTK	DGRIKPD	VMAPGTFFILSARSSLPDSSF 240
DB	181	TVGATENLR	PSFGSYADN	INHVAQF	SSRGPTK	DGRIKPD	VMAPGTFFILSARSSLPDSSF 240
QY	241	WANHDSKYA	YMGGTSMAT	PIVAGNVA	QRLREHFV	KNRGIT	TPKPSLLKAALIAAGADIGLGY 300
DB	241	WANHDSKYA	YMGGTSMAT	PIVAGNVA	QRLREHFV	KNRGIT	TPKPSLLKAALIAAGADIGLGY 300
QY	301	PNGNGWGR	VTLDKSL	NVAYVNESS	SLSTSQAT	YSFTAT	AGPKPLKISLVMSDAPASTTA 360
DB	301	PNGNGWGR	VTLDKSL	NVAYVNESS	SLSTSQAT	YSFTAT	AGPKPLKISLVMSDAPASTTA 360
QY	361	SVTLVNDL	DLVITAP	NGTQYV	GNDFTS	PDNDWGR	NNVNFVINAPOSQYTTIEVQAYN 420
DB	361	SVTLVNDL	DLVITAP	NGTQYV	GNDFTS	PDNDWGR	NNVNFVINAPOSQYTTIEVQAYN 420
QY	421	VPVGPQT	FSLAIVN	434			
DB	421	VPVGPQT	FSLAIVN	434			

RESULT 2

US-10-385-662-2

; Sequence 2, Application US/10385662
; Publication No. US20040002432A1
; GENERAL INFORMATION:
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: SAITO, KAZUHIRO
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: IZAWA, YOSHIFUMI
; APPLICANT: SAEKI, KATSUHISA
; APPLICANT: KOBAYASHI, TOHRU
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: Alkaline protease
; FILE REFERENCE: 234938US0
; CURRENT APPLICATION NUMBER: US/10/385,662
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: JP 2002-081428
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: JP 2002-165987
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: JP 2002-304230
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: JP 2002-304231
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-385-662-2

Query Match 100.0%; Score 2247; DB 4; Length 434;

Best Local Similarity 100.0%; Pred. No. 3.6e-171;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	NDVARGIVKADVAGSSYGLYGQGI	VADVADTGLD	GRNDSSMH	EAFRGKIT	ALYALGR	TN 60
DB	1	NDVARGIVKADVAGSSYGLYGQGI	VADVADTGLD	GRNDSSMH	EAFRGKIT	ALYALGR	TN 60
QY	61	NANDTNGHGT	HVAGSVLNGST	TKGMAPOANL	VFQSI	MDSGGGLG	PSNLQTLFSQAYS 120
DB	61	NANDTNGHGT	HVAGSVLNGST	TKGMAPOANL	VFQSI	MDSGGGLG	PSNLQTLFSQAYS 120
QY	121	AGARIHTNSGAA	VNGAYTTDS	RNVDDYVR	KNDMTIL	FAAGNEGP	NGGTISAPGTAKNAI 180
DB	121	AGARIHTNSGAA	VNGAYTTDS	RNVDDYVR	KNDMTIL	FAAGNEGP	NGGTISAPGTAKNAI 180
QY	181	TVGATENLR	PSFGSYADN	INHVAQF	SSRGPTK	DGRIKPD	VMAPGTFFILSARSSLPDSSF 240
DB	181	TVGATENLR	PSFGSYADN	INHVAQF	SSRGPTK	DGRIKPD	VMAPGTFFILSARSSLPDSSF 240
QY	241	WANHDSKYA	YMGGTSMAT	PIVAGNVA	QRLREHFV	KNRGIT	TPKPSLLKAALIAAGADIGLGY 300
DB	241	WANHDSKYA	YMGGTSMAT	PIVAGNVA	QRLREHFV	KNRGIT	TPKPSLLKAALIAAGADIGLGY 300
QY	301	PNGNGWGR	VTLDKSL	NVAYVNESS	SLSTSQAT	YSFTAT	AGPKPLKISLVMSDAPASTTA 360
DB	301	PNGNGWGR	VTLDKSL	NVAYVNESS	SLSTSQAT	YSFTAT	AGPKPLKISLVMSDAPASTTA 360
QY	361	SVTLVNDL	DLVITAP	NGTQYV	GNDFTS	PDNDWGR	NNVNFVINAPOSQYTTIEVQAYN 420
DB	361	SVTLVNDL	DLVITAP	NGTQYV	GNDFTS	PDNDWGR	NNVNFVINAPOSQYTTIEVQAYN 420
QY	421	VPVGPQT	FSLAIVN	434			
DB	421	VPVGPQT	FSLAIVN	434			

RESULT 3

US-10-456-479-2

; Sequence 2, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:

; APPLICANT: SATO, TSUYOSHI
 ; APPLICANT: OKUDA, MITSUYOSHI
 ; APPLICANT: TAKIMURA, YASUSHI
 ; APPLICANT: SUMITOMO, NOBUYUKI
 ; APPLICANT: KOBAYASHI, TOHRU
 ; APPLICANT: KOBAYASHI, TOHRU
 ; TITLE OF INVENTION: ALKALINE PROTEASE
 ; FILE REFERENCE: 238700US0
 ; CURRENT APPLICATION NUMBER: US/10/456,479
 ; CURRENT FILING DATE: 2003-06-09
 ; PRIOR APPLICATION NUMBER: JP 2002-186387
 ; PRIOR FILING DATE: 2002-06-26
 ; PRIOR APPLICATION NUMBER: JP 2002-304232
 ; PRIOR FILING DATE: 2002-10-18
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 434
 ; TYPE: PRT
 ; ORGANISM: Bacillus sp. KSM-KP43
 US-10-456-479-2

Query Match 100.0%; Score 2247; DB 4; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.6e-171;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
 Db 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60

 Qy 61 NNDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSOAYS 120
 Db 61 NNDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSOAYS 120

 Qy 121 AGARIHTNSWGAANGVAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
 Db 121 AGARIHTNSWGAANGVAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

 Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFTLSARSSLPDSSF 240
 Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFTLSARSSLPDSSF 240

 Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300
 Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300

 Qy 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
 Db 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360

 Qy 361 SVTLVNDLDLIVITAPNGTQYVGNDFTPYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
 Db 361 SVTLVNDLDLIVITAPNGTQYVGNDFTPYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420

 Qy 421 VPVGQPTFSLAIVN 434
 Db 421 VPVGQPTFSLAIVN 434

RESULT 4
 US-10-837-566-1
 ; Sequence 1, Application US/10837566
 ; Publication No. US20040203129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HATADA, YUJI
 ; APPLICANT: OGAWA, AKINORI
 ; APPLICANT: KAGEYAMA, YASUSHI
 ; APPLICANT: SATO, TSUYOSHI
 ; APPLICANT: ARAKI, HIROYUKI
 ; APPLICANT: SUMITOMO, NOBUYUKI
 ; APPLICANT: OKUDA, MITSUYOSHI
 ; APPLICANT: SAEKI, KATSUHIISA
 ; TITLE OF INVENTION: Alkaline proteases

; FILE REFERENCE: 215483US0
 ; CURRENT APPLICATION NUMBER: US/10/837,566
 ; CURRENT FILING DATE: 2004-05-04
 ; PRIOR APPLICATION NUMBER: US/09/985,689A
 ; PRIOR FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: JP P2000-355166
 ; PRIOR FILING DATE: 2000-11-22
 ; PRIOR APPLICATION NUMBER: JP P2001-114048
 ; PRIOR FILING DATE: 2001-04-12
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 434
 ; TYPE: PRT
 ; ORGANISM: Bacillus sp.
 US-10-837-566-1

Query Match 100.0%; Score 2247; DB 4; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.6e-171;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
 Db 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60

 Qy 61 NNDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSOAYS 120
 Db 61 NNDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSOAYS 120

 Qy 121 AGARIHTNSWGAANGVAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
 Db 121 AGARIHTNSWGAANGVAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

 Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFTLSARSSLPDSSF 240
 Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFTLSARSSLPDSSF 240

 Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300
 Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300

 Qy 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
 Db 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360

 Qy 361 SVTLVNDLDLIVITAPNGTQYVGNDFTPYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
 Db 361 SVTLVNDLDLIVITAPNGTQYVGNDFTPYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420

 Qy 421 VPVGQPTFSLAIVN 434
 Db 421 VPVGQPTFSLAIVN 434

RESULT 5
 US-10-820-712A-1
 ; Sequence 1, Application US/10820712A
 ; Publication No. US20050026804A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KAO CORPORATION
 ; APPLICANT: Okuda, Mitsuyoshi
 ; APPLICANT: Izawa, Yoshifumi
 ; APPLICANT: Kobayashi, Tohru
 ; APPLICANT: Koyama, Shingo
 ; APPLICANT: Sato, Tsuyoshi
 ; TITLE OF INVENTION: ALKALINE PROTEASE
 ; FILE REFERENCE: 251701-US0
 ; CURRENT APPLICATION NUMBER: US/10/820,712A
 ; CURRENT FILING DATE: 2004-04-09
 ; PRIOR APPLICATION NUMBER: 2003-106708
 ; PRIOR FILING DATE: 2003-04-10
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-712A-1

Query Match      100.0%; Score 2247; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Qy 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPTFTILSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPTFTILSARSSLAPDSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
Qy 301 PNGNGWGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNGWGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLDELVITAPNGTQYVGNDFTSYNDNDGRNNVNFVINAPOSQGTYYTIEVQAYN 420
Db 361 SVTLVNDLDELVITAPNGTQYVGNDFTSYNDNDGRNNVNFVINAPOSQGTYYTIEVQAYN 420
Qy 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 6
US-10-820-714A-1
; Sequence 1, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Kobayashi, Tōhru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697US0
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-714A-1

Query Match      100.0%; Score 2247; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Qy 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPTFTILSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPTFTILSARSSLAPDSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
Qy 301 PNGNGWGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNGWGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLDELVITAPNGTQYVGNDFTSYNDNDGRNNVNFVINAPOSQGTYYTIEVQAYN 420
Db 361 SVTLVNDLDELVITAPNGTQYVGNDFTSYNDNDGRNNVNFVINAPOSQGTYYTIEVQAYN 420
Qy 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 7
US-09-920-954-6
; Sequence 6, Application US/09920954
; Publication No. US20020064854A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-6

Query Match      100.0%; Score 2247; DB 3; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 266
Qy 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
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Db 267 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARIHTNSWGAANGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAAGTFFILSARSSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAAGTFFILSARSSSLAPDSSF 446
Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIIGLY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIIGLY 506
Qy 301 PNGNQGWGRVTLDSKLNVAAYVNESSSLSTSOKATYSTATAGKPLKISLWSDAPASTTA 360
Db 507 PNGNQGWGRVTLDSKLNVAAYVNESSSLSTSOKATYSTATAGKPLKISLWSDAPASTTA 566
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDRNNVENVFINAPQSGTYYTIEVOAYN 420
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIIGLY 506
Qy 301 PNGNQGWGRVTLDSKLNVAAYVNESSSLSTSOKATYSTATAGKPLKISLWSDAPASTTA 360
Db 507 PNGNQGWGRVTLDSKLNVAAYVNESSSLSTSOKATYSTATAGKPLKISLWSDAPASTTA 566
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDRNNVENVFINAPQSGTYYTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDRNNVENVFINAPQSGTYYTIEVOAYN 626
Qy 421 VPVGPOTFSLAIVN 434
Db 627 VPVGPOTFSLAIVN 640
RESULT 8
US-10-456-479-4
; Sequence 4, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NORIYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700U50
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR FILING DATE: 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR FILING DATE: 2002-304232
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-456-479-4

Query Match 100.0%; Score 2247; DB 4; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 266
Qy 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARIHTNSWGAANGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAAGTFFILSARSSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAAGTFFILSARSSSLAPDSSF 446
Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIIGLY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIIGLY 506

Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIIGLY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIIGLY 506
Qy 301 PNGNQGWGRVTLDSKLNVAAYVNESSSLSTSOKATYSTATAGKPLKISLWSDAPASTTA 360
Db 507 PNGNQGWGRVTLDSKLNVAAYVNESSSLSTSOKATYSTATAGKPLKISLWSDAPASTTA 566
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDRNNVENVFINAPQSGTYYTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDRNNVENVFINAPQSGTYYTIEVOAYN 626
Qy 421 VPVGPOTFSLAIVN 434
Db 627 VPVGPOTFSLAIVN 640
RESULT 9
US-10-784-870-6
; Sequence 6, Application US/10784870
; Publication No. US20040142837A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/10/784,870
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/509,814A
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-784-870-6

Query Match 100.0%; Score 2247; DB 4; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 266
Qy 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARIHTNSWGAANGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAAGTFFILSARSSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAAGTFFILSARSSSLAPDSSF 446
Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIIGLY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIIGLY 506

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Qy 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVINAPOSQGTITIEVQAYN 420
Db 567 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVINAPOSQGTITIEVQAYN 626

Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

RESULT 10
US-10-820-712A-3
; Sequence 3, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Izawa, Yoshihumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-USO
; CURRENT APPLICATION NUMBER: US/10/820,712A
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-712A-3

Query Match 100.0%; Score 2247; DB 5; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVQAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRKITALYALGRTN 60
Db 207 NDVARGIVKADVQAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRKITALYALGRTN 266

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHTNSWGAANVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFILSARSSLPDSSF 446

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 506

Qy 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVINAPOSQGTITIEVQAYN 420
Db 567 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVINAPOSQGTITIEVQAYN 626

Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
```

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RESULT 11
US-10-820-714A-3
; Sequence 3, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697USO
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-714A-3

Query Match 100.0%; Score 2247; DB 5; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVQAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRKITALYALGRTN 60
Db 207 NDVARGIVKADVQAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRKITALYALGRTN 266

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHTNSWGAANVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFILSARSSLPDSSF 446

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 506

Qy 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVINAPOSQGTITIEVQAYN 420
Db 567 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVNFVINAPOSQGTITIEVQAYN 626

Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

RESULT 12
US-10-456-479-11
; Sequence 11, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI
```

```
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700US0
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP9865
US-10-456-479-11

Query Match          99.8%; Score 2242; DB 4; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAOSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAOSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
Qy 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSAAYS 120
Db 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSAAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPOGTFILSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPOGTFILSARSSLAPDSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALTAGAADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALTAGAADIGLY 300
Qy 301 PNGNQGRVTLDKSLNVAAYVNESSSLSTSOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNQGRVTLDKSLNVAAYVNESSSLSTSOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYYTIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYYTIEVOAYN 420
Qy 421 VPVGPOTFSLAIVN 434
Db 421 VPVGPOTFSLAIVN 434

RESULT 13
US-10-820-712A-14
; Sequence 14, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-US0
; CURRENT APPLICATION NUMBER: US/10/820,712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR FILING DATE: 2003-106708
; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-712A-15

Query Match          99.8%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-712A-14

Query Match          99.8%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasuhide
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697US0
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-714A-15

Query Match          99.8%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVADVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVADVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 300
Qy 301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTYYTIEVQAYN 420
Db 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTYYTIEVQAYN 420
Qy 421 VPVGPQTFFSLAIVN 434
Db 421 VPVGPQTFFSLAIVN 434
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RESULT 15

```
US-09-920-954-8
; Sequence 8, Application US/09920954
; Publication No. US20020064854A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGIYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PR1
; ORGANISM: Bacillus sp.
US-09-920-954-8
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Query Match          99.8%; Score 2242; DB 3; Length 640;
Best Local Similarity 99.8%; Pred. No. 1.5e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVADVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVADVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
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Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 446
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 506
Qy 301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGNQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 566
Qy 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTYYTIEVQAYN 420
Db 567 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTYYTIEVQAYN 626
Qy 421 VPVGPQTFFSLAIVN 434
Db 627 VPVGPQTFFSLAIVN 640
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Search completed: March 30, 2006, 08:37:41

Job time : 167 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2006, 08:35:01 ; Search time 25 Seconds
(without alignments)

528.471 Million cell updates/sec

Title: US-10-820-712A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVOAYNPVPGQTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 100 summaries

Database :

Published Applications AA New:*

- 1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /SIDSS/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	285.5	12.8	802	6	US-10-510-386-2
2	253	11.3	874	6	US-10-510-386-28
3	253	11.3	1047	6	US-10-510-386-200
4	245	10.9	272	7	US-11-020-602-236
5	240	10.7	269	7	US-11-020-602-6
6	235.5	10.5	275	7	US-11-065-943-54
7	235.5	10.5	275	7	US-11-020-602-3
8	231.5	10.3	274	7	US-11-156-062-14
9	230.5	10.3	274	7	US-11-156-062-12
10	230.5	10.3	379	7	US-11-156-062-23
11	229.5	10.2	274	7	US-11-020-602-5
12	226.5	10.1	274	7	US-11-156-062-4
13	226.5	10.1	274	7	US-11-156-062-8
14	225.5	10.0	274	7	US-11-156-062-10
15	225.5	10.0	274	7	US-11-020-602-208
16	224.5	10.0	274	7	US-11-156-062-6
17	223.5	9.9	275	7	US-11-020-602-4
18	223.5	9.9	274	7	US-11-156-062-16
19	221.5	9.9	274	7	US-11-156-062-18
20	220.5	9.8	274	7	US-11-156-062-2
21	219.5	9.8	382	7	US-11-020-602-2
22	209.5	9.3	280	7	US-11-020-602-209
23	205	9.1	1432	6	US-10-510-386-218
24	203	9.0	1647	7	US-11-052-554A-260
25	181	8.1	740	7	US-11-096-568A-24714

Sequence 24713, A
Sequence 24712, A
Sequence 22, Appl
Sequence 31863, A
Sequence 31862, A
Sequence 31861, A
Sequence 17896, A
Sequence 17895, A
Sequence 17894, A
Sequence 24028, A
Sequence 24027, A
Sequence 24026, A
Sequence 31251, A
Sequence 23983, A
Sequence 23982, A
Sequence 2, Appl
Sequence 1176, Ap
Sequence 11252, A
Sequence 1245, Ap
Sequence 23984, A
Sequence 284, App
Sequence 3, Appl
Sequence 361, App
Sequence 142, App
Sequence 31253, A
Sequence 82, Appl
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Sequence 268, App
Sequence 44, Appl
Sequence 45, Appl
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Sequence 160, App
Sequence 7824, App
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Sequence 7521, Ap
Sequence 31963, A
Sequence 31962, A
Sequence 13, Appl
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Sequence 4, Appl
Sequence 341, App
Sequence 42, Appl
Sequence 212, App
Sequence 9, Appl
Sequence 91, Appl
Sequence 809, App
Sequence 32, Appl
Sequence 160, App

99 104 4.6 355 7 US-11-222-451-2 Sequence 2, Appli
100 104 4.6 639 7 US-11-052-554A-165 Sequence 165, App

ALIGNMENTS

RESULT 1
US-10-510-386-2

; Sequence 2, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-2

Query Match 12.8%; Score 286.5; DB 6; Length 802;
Best Local Similarity 23.0%; Pred. No. 3.9e-13;
Matches 143; Conservative 69; Mismatches 178; Indels 231; Gaps 27;
QY 2 DVARGIVKADVAQSSYGLYGOQIVAVADTGLDTRND--SSMHEAFROK--ITALYALGR 58
DB 158 DKSAPPFAGDAQWKS-GYTGKGIKVAVIDTGVYTHPDLKNNFGPYKGYDFVNDYDQ 216
QY 59 TNNANDTNG---HGHVHAGSVLNGSTNKGMAPQANLVFQIMDSGGGLGLPSNLQTLF 115
DB 217 TPTGDPGRGATDHGHVHAGTAAAGQI-KGVAPEATLLAYRLVLPFGG--SGTTENVIAGI 273
QY 116 SQAYSAGARIHTNSGAAVNGA-YTTDSRNVDVYKNDMTILPAAGNEGPNGGTISAPG 174
DB 274 EKAVADGAKVMNLGNSLNSPDYATSI--ALDWAAGVAVTSGNSGPNWTVGSPG 331
QY 175 TAKNAITVGAIE---NLRPSFGS----- 194
DB 332 TSVRAISVGASQLPYNEYSVTLPSSYSAKVMGYQBEKDLEALNGQVELVEAGLQADDF 391
QY 195 -----YADNINH----- 201
DB 392 SGKVKGVAVIQRVIPFVDKAENAKNAGAIGAVIYNNATGEIBANVMGMVAVPTVKLSK 451
QY 202 -----VAQFSSRGPTKD-GRIPKDVMAAGTFFILSA 230
DB 452 EGEKLVQIQEKGKHSVVFSLDKKLGETIASFSRGPVMDTWIMKPDVSPAGVNIYST 511
QY 231 RSSLAPDSSFANHDSK-----YAYMGGTSMATPIVAGNVAQLREHFVKNRGITP--KPSL 284
DB 512 IPT-----HDPKPNPYGSGKGTSMASPHVAGTAAILKQ-----AKPDWTPEQ 554
QY 285 LKAALIAGNADI-----GLQYPNGNQGWRTLDKSLNVAYNVNESS----- 326
DB 555 IKGVLMTAEKLTDENGKPLPNTQAGSIRIMEALKASSIVTPGSHSYGTFLDKDKGQKT 614
QY 327 -----LSTSQKA-----TYGFTATAGKPLKISLVMSD-----APASTT---ASVTILVNDL 368
DB 615 KQQAFTIENLSHRKAYQLEYFKGTG-----ITVSGTERVVVPANQTCGAAKVTVNSA 669
QY 369 DLVITAPNGTQVGNDFTSPPYNNWDGRNVE---NVFINAP-----QSGT 411
DB 670 KTKAGTYEGTVIREE-----DGRKVAEITPLILVKEPDYPRVTSVTVEPGAKQGA 719

QY 412 YTIEVQAYNVYPVGPQTFTSLAI 432
DB 720 YTIE--AY-LPGGAELAFILV 737

RESULT 2

US-10-510-386-28
; Sequence 28, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 874
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-28

Query Match 11.3%; Score 253; DB 6; Length 874;
Best Local Similarity 27.2%; Pred. No. 1.2e-10;
Matches 95; Conservative 51; Mismatches 129; Indels 74; Gaps 13;
QY 25 IVAVADTGLDTRNDSSMHEAFRCKI---TALYALGRITNNANDTNGHGHVHAGSVLG--- 78
DB 447 VIADVDTGVDTLADLS-----GSVKDEGYNTVGTADAMDNGHGHVHAGSVLG--- 500
QY 79 NGSTNKGMAPQANLVFQIMDSGGGLGLPSNLQTLFSQAYSAGARIHTNSGAAVNGAY 138
DB 501 NHFSMAGINAYAKTILPVKVLDSG--SGDTEQIANGIYYAADHCAKVINLSLG---GPY 554
QY 139 TDSRNVDVYKNDMTILFAAGNEGPNGGTISAPGAKNAITVGAENLPPSPGSGYADN 198
DB 555 SRVMEYALKYAASKNVTIVAATGNDGVS--EISYPASSKYTLTSLVGCATNNL----- 602
QY 199 INHVAQSSRGPTKDGRIKPDVMAAGTFFILSARSLAPDSSFANHDSKYAYMGGTSMAT 258
DB 603 -DLVSDYSNYGKGL-----DMVAPGTDI-----PSLVPDGN-----VTYMSGTSM 643
QY 259 PIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADIGL---GYPNGN----- 304
DB 644 PHVAAAAGLL-----LSQNPSPKPKQIASLLTETTADVAFEEQNPDPDYDLIEPAAQI 698
QY 305 -----QGWGRVTLDKSLNVAYNVNESSLSQTSQKATYSFTATAGKPLKI 347
DB 699 PGYDFVSGWRLNVFHAASVPELNKMHVPILNRHTTAVTGTAKSGVTVKI 747

RESULT 3

US-10-510-386-200
; Sequence 200, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200

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; LENGTH: 1047
; TYPE: FRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-200

Query Match          11.3%; Score 253; DB 6; Length 1047;
Best Local Similarity 27.2%; Pred. No. 1.5e-10;
Matches 95; Conservative 51; Mismatches 129; Indels 74; Gaps 13;

Qy      25   IVAVADTGLDGRNDSSMHEAFRGKI---TALYALGRTNNANDNTNGHGVACSVLG--- 78
Db      447   VVVVDVTGVDTHTLADLS-----GSVKKDEGYNVVGTADAMDNDGGHTHVSGIIAAQD 500

Qy      79   NGSTNKGMAPQANLVFOSIMDSGGGLGPLSNLQTLFSQAYSAGARLHTNSWGAANVGAY 138
Db      501   NHFSMAGINAYAKILPVKVLDDSG--SGDTEQIANGTIYAADHCAKVNLISLG---GPY 554

Qy      139  TTDSRNVDVYRKNDMTILFAAGNEGPNGGTISAPGTAKNAITYGATENLRPFGSVADN 198
Db      555   SRVMEYALKYAAKNVTIVATGNDGVS--EISYPASSKYTVLSVGTANNL----- 602

Qy      199  INHVAQFSRRGPTKDGRIPKPDVMAPGTFILSARSSLAPDSPSFWANHDSKYAYMGTSMAT 258
Db      603   -DLVSDSYNYGKGL-----DMVAPGTDI-----PSLVPDGN-----VTYMSGTSMAA 643

Qy      259  PIVAGNVAQAREHFVNKGRIPTPKSLLLKAALIAGAADIQL---GYPNGN----- 304
Db      644   PHVAAAAGL-----LSQNPLKPKQIASLLTETTTADVAFEEQNPNPDVLDIEPAAQI 698

Qy      305  -----QCWGRVTLDKSLNAVYNNESSLSOKATYSFTATAGPLKI 347

Db      699  PGYDFVSGWRGLNVFYHAASVPFLNMKVHPVILNRHTAVTGTAKSQGVTKI 747
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RESULT 4
US-11-020-602-236
; Sequence 236, Application US/11020602
; Publication No. US20060024764A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME
; FILE REFERENCE: GC527C2
; CURRENT APPLICATION NUMBER: US/11/020,602
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 236
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid of
; OTHER INFORMATION: Bacillus lentus and Bacillus amyloliquefaciens
US-11-020-602-236

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Qy 126 HTNSWGAANGVAYTDSRNVDDYVRKNDMTILFAAGNEGNG--GTISAPGTAKNAITVG 183
      ||| : ||| : : : ||||| : ||| : ||| : |||
Db 120 INMSLGGSGSAAL-----KAAVDKAVASGVVVVAAAGNEGTSGSSSTVGYPGKYPVIAVG 175
      ||| : ||| : : : ||||| : ||| : ||| : |||
Qy 184 ATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTILSARSSSLAPDSSFWAN 243
      ||| : ||| : : : ||||| : ||||| : ||| : |||
Db 176 A-----VDSSNRQSFSSVGP-----ELDVMAPG-----VSIQSTLP----- 207
      ||| : ||| : : : ||||| : ||||| : ||| : |||
Qy 244 HDISKYAMGGSMTATPIVANGVA 266
      :|| ||||| : |||
Db 208 -GNKYGAYNGTSMASPHVAGAAA 229
      :|| ||||| : |||

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RESULT 5
 US-11-020-602-6
 ; Sequence 6, Application US/11020602
 ; Publication No. US20060024764A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Estell, David
 ; APPLICANT: Harding, Fiona
 ; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
 ; TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME
 ; FILE REFERENCE: GC527C2
 ; CURRENT APPLICATION NUMBER: US/11/020,602
 ; CURRENT FILING DATE: 2004-12-22
 ; PRIOR APPLICATION NUMBER: US 09/500,135
 ; PRIOR FILING DATE: 2000-02-08
 ; PRIOR APPLICATION NUMBER: US 09/060,872
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 240
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 269
 ; TYPE: PRT
 ; ORGANISM: Bacillus lentus
 US-11-020-602-6

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RESULT 6
US-11-065-943-54
; Sequence 54, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-156-062-8

Query Match      10.1%; Score 226.5; DB 7; Length 274;
Best Local Similarity 29.5%; Pred. No. 2.2e-09;
Matches 85; Conservative 36; Mismatches 100; Indels 67; Gaps 12;

Qy 7 IVKADVAQSSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRNTNANDTN 66
Db 10 LIKADKVQAO-GFKGANVKVAVLDGTGQASHPLDNLVVG-----ASPVAGEAYNA-DGN 61
Qy 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFQSIMDS--GGGLGGLPSNLQTLFSQ----- 117
Db 62 GHGTHVAGTVAALDNTTGVLGVPVSLYAVKVLNSSGSGSYGIVSGIEWATTNDMDVI 121
Qy 118 AYSAGARIHTNSGAAVNGAYTTDSNRVDDYVRKNMDTILFAAGNEGPNG--GTISAPGT 175
Db 122 NMSLGGASGSTAMKQAVDNAYA-----RGVVVVAAGNSGSGTNTTIGYPAK 169
Qy 176 AKNAITVYATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILLSARSLA 235
Db 170 YDSVIAVGA-----VDSNNSRASFSVG-----AELEVMAFGAGVYSTYPT-- 210
Qy 236 PDSSFWANHDSKYAYMGTSMTPIVAGNVA-----QLREHFVKNR 276
Db 211 -----NTYATWDGTSMAHPHVGAAALILSKHPNLSASQVRNR 248

RESULT 14
US-11-156-062-10
; Sequence 10, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITISIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US/11/156,062
; PRIOR FILING DATE: 2003-12-20
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-156-062-10

Query Match      10.0%; Score 225.5; DB 7; Length 274;
Best Local Similarity 30.2%; Pred. No. 2.6e-09;
Matches 85; Conservative 36; Mismatches 107; Indels 53; Gaps 11;

Qy 7 IVKADVAQSSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRNTNANDTN 66
Db 10 LIKADKVQAO-GFKGANVKVAVLDGTGQASHPLDNLVVG-----ASPVAGEAYNA-DGN 61
Qy 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYSAGAR 124
Db 62 GHGTHVAGTVAALDNTTGVLGVPVSLYAVKVLNSSG--SGSYSGIVSGIEWATTNGMD 119
Qy 125 IHTNSGAAVNGAYTTDSNRVDDYVRKNMDTILFAAGNEGPNG--GTISAPGTAKNAITV 182
Db 120 VINSLGGA---SGSTAMKQAVDNAYARGVVVVAAGNSGSGTNTTIGYPAKYDSVIAV 176
Qy 183 GATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILLSARSLAPDSSFWA 242
Db 177 GA-----VDSNNSRASFSVG-----AELEVMAFGAGVYSTYPT----- 210
Qy 243 NHDSKYAYMGTSMTPIVAGNVA-----QLREHFVKNR 276
Db 211 ---NTYATWDGTSMAHPHVGAAALILSKHPNLSASQVRNR 248

RESULT 13
US-11-156-062-8
; Sequence 8, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITISIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US/11/156,062
; PRIOR FILING DATE: 2003-12-20
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2006, 08:29:31 ; Search time 41 Seconds
(without alignments)
1018.490 Million cell updates/sec

Title: US-10-820-712A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAYNVPGQTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523.5	23.3	1743	2	T18279
2	497	22.1	1905	2	T18267
3	347.5	15.5	444	2	B83891
4	320.5	14.3	442	2	A69587
5	310.5	13.8	806	2	A41341
6	302.5	13.5	1398	2	T28159
7	283	12.6	580	2	S11890
8	281	12.5	419	1	S25835
9	280	12.5	799	2	G83753
10	279.5	12.4	1345	2	T29090
11	277	12.3	420	1	J23407
12	267	11.9	715	2	G34908
13	263	11.7	1331	2	A72647
14	259.5	11.5	757	2	C84120
15	257.5	11.5	513	1	A35742
16	253.5	11.3	894	2	F69730
17	251	11.2	627	2	D75393
18	246.5	11.0	402	1	JU0173
19	246.5	11.0	534	1	JU0332
20	243	10.8	519	2	S71451
21	242.5	10.8	401	2	I39974
22	240	10.7	380	2	A49778
23	240	10.7	488	2	A11930
24	235.5	10.5	382	1	SUBSN
25	235	10.5	378	2	A33973
26	235	10.5	382	2	I39780
27	234	10.4	910	2	C69456
28	234	10.4	1374	2	D72593
29	232.5	10.3	525	2	G84406

30	231	10.3	321	1	S27501
31	230.5	10.3	379	1	SUBSCL
32	229.5	10.2	601	2	JC4576
33	227	10.1	1167	1	A35066
34	226.5	10.1	1118	2	H97298
35	225.5	10.0	381	2	JH0778
36	225.5	10.0	613	2	S75976
37	225.5	10.0	1052	2	T17093
38	223.5	9.9	381	1	SUBSI
39	223.5	9.9	381	1	SUBSS
40	223.5	9.9	381	2	JQ1487
41	222.5	9.9	275	2	JC1085
42	222	9.9	384	2	JC4802
43	221.5	9.9	272	2	A23624
44	221.5	9.9	530	2	A42605
45	221	9.8	1036	2	JC5568
46	220.5	9.8	769	2	D86335
47	218.5	9.7	535	2	B82358
48	217	9.7	733	2	F75384
49	216.5	9.6	274	1	SUBSD
50	216.5	9.6	361	2	A48373
51	216.5	9.6	645	1	SUBSMP
52	215	9.6	319	2	I39866
53	215	9.6	323	2	I39867
54	215	9.6	706	2	T01351
55	214.5	9.5	361	2	G83756
56	214	9.5	279	1	SUMVTV
57	214	9.5	293	2	JQ0380
58	214	9.5	326	1	C41335
59	214	9.5	409	1	S32905
60	211.5	9.4	1052	2	H83909
61	211	9.4	905	2	F82734
62	210	9.3	374	2	I39781
63	210	9.3	731	1	A55800
64	209.5	9.3	1433	1	A36734
65	209	9.3	401	2	A57690
66	208.5	9.3	388	1	S22387
67	208	9.3	387	2	S11985
68	208	9.3	467	1	S45493
69	207.5	9.2	1034	2	JC5569
70	204.5	9.1	1902	1	B44858
71	203.5	9.1	603	2	S27055
72	202.5	9.0	328	2	G95392
73	202	9.0	1736	2	T05174
74	201	8.9	1902	2	B45764
75	200	8.9	403	1	SUASO
76	200	8.9	403	2	JC7081
77	200	8.9	533	1	JU0146
78	199.5	8.9	440	2	H72784
79	199.5	8.9	910	2	H82826
80	199.5	8.9	1374	2	T16129
81	199.5	8.9	1448	2	AI2007
82	199	8.9	384	1	SUTIKA
83	197.5	8.8	772	2	T05838
84	197	8.8	753	2	B96687
85	197	8.8	756	2	T04187
86	196.5	8.7	321	2	JC5460
87	196	8.7	1946	2	JC6032
88	195.5	8.7	775	2	T00962
89	195.5	8.7	779	2	T07170
90	195	8.7	322	2	G83922
91	195	8.7	397	2	JC7208
92	194.5	8.7	1902	2	S06997
93	194	8.6	372	2	D83735
94	194	8.6	1396	2	T10627
95	193.5	8.6	615	2	AH2248
96	192.5	8.6	454	2	T43069
97	192.5	8.6	801	2	T07617
98	192.5	8.6	1962	2	A32634
99	192	8.5	403	1	S22184
100	192	8.5	461	2	A70837

alkaline proteinase
subtilisin (EC 3.4
serine proteinase
streptococcal Csa
subtilisin like pr
subtilisin (EC 3.4
hypothetical prote
intraluminal subti
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subtilisin (EC 3.4
halolysin (EC 3.4.
serine proteinase
T20H2.6 protein -
alkaline serine pr
serine proteinase,
subtilisin (EC 3.4
high-alkaline seri
serine proteinase
microbial serine p
microbial serine p
subtilisin-like pr
subtilisin-type al
thermitase (EC 3.4
protease T (EC 3
microbial serine p
serine proteinase
cell wall-associat
serine proteinase
subtilisin (EC 3.4
cucumisin (EC 3.4.
bactillopeptidase F
aerolysin precursor
cuticle-degrading
serine proteinase
serine proteinase
serine proteinase
lactocepin (EC 3.4
basic serine prote
probable protease
hypothetical prote
lactocepin (EC 3.4
oryzin (EC 3.4.21.
oryzin (EC 3.4.21.
serine proteinase
probable alkaline
serine proteinase
serine proteinase
hypothetical prote
Subtilase family p
endopeptidase K (E
subtilisin-like pr
subtilisin-like pr
subtilisin-like pr
intracellular alka
lactocepin (EC 3.4
hypothetical prote
subtilisin-like pr
intracellular alka
allergen Pen-n-13
lactocepin (EC 3.4
subtilisin-type al
hypothetical prote
proteinase [import
probable serine pr
proteinase TMP - t
lactocepin (EC 3.4
oryzin (EC 3.4.21.
probable proteinase

ALIGNMENTS

RESULT 1

multidrug resistance transport protein - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18279

R;Shaulsky, G.; Loomis, W.F.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z18855
A:Accession: T18279

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1743 <SHA>

A:Cross-references: UNIPROT:Q23868; UNIPARC:UPI000013687D; EMBL:U60086; NID:gi399914; P18267

C:Genetics:

A:Gene: tagC

Query Match 23.3%; Score 523.5; DB 2; Length 1743;
Best Local Similarity 27.9%; Pred. No. 3.5e-25;
Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;

```
Qy 19 LYGGQIIVAVADTGLDTCR---NDS-----SMHEAFRGKITALYALGRNTNANDTNGH 68
Dy 314 LRGGQILSIADTGLDGHCFSSKYPPIPLNSVNLNHR-KVYYITSTSDSDSKVDGH 372
Qy 69 GTHVAGSVLG-----NGSTNKGMAPQANLVFQSIMDSGGGLGGL--PSNLQTLFSGAY 119
Dy 373 GTHICGSAAGTPEDSSVNISSFSGLATDAKIAF---FDLASGSSSLTPPSDLKQLYQPLY 429
Qy 120 SAGARIHTNSWGA---AVNGAYTTDSRNVDYVRKN-DWMTILFAAGNEGPNGGTIS--A 172
Dy 430 DAGARVHCDSGSVSGVEGTSYSDTASIDDFLTFPHDFILRAAGN---NEQVLSLT 486
Qy 173 PGTAKNATVGCATENLR-----PSFGSYADNI-----YADNI----- 199
Dy 487 QSTAKNVITVGAHQTHENYLTGDPNYINYQSSVDINQELICDFDSRYCNVTTAQCCLES 546
Qy 200 -----NHVAQFSRSGPTKDGRIKPDVMAFGTFIL 228
Dy 547 NATTLGASCCPTLLRKSVIDAANTQPLLYNENNICSFSKGPETHDGRMKPALVAPGEYIT 606
Qy 229 SARSSLA-----PDSSFWANHDSKIYMGTSMATPIVAGNVAQLRHF-----F 272
Dy 607 SARSGNANTTDQCGDGL-PNTNALLA-ISGTSMATSPAAAATTLIRQYLVGDGYPTGSI 664
Qy 273 VKNRGITPKPSLLKAALTAGA-----ADTGLGYPNGN-----QGWGRVT 311
Dy 665 VESNKLQPTGSLLKALMINNAQLNGTFLQITSSITYPSNQVFNFAGASLVQVGAI 724
Qy 312 LDKSLNVAVYNESS-----SLSTSOKATYSFT-- 338
Dy 725 MSNHLHVNNNNNNNNKTSIDGITKFDGIGGLDLVLKVPQWKEBSLSTGQNTSCFYTK 784
Qy 339 -----ATAGKPLK--ISLWSDAPASTASVTLVNDLDLVI-----TAPNGT 378
Dy 785 PSSSSSSNGNNIPRVATLVMTDPPSYAGAKFNLVNLDLMTIYYRDNGSTIFYSNOGGS 844
Qy 379 QYVGNDFTSFYNDWGRNVENVINAPQSGTYTIEVQAVNPVGPQTES 429
Dy 845 SFLLG---LAPTDQT---LNNVEGIVHNPTPEPTMYRFMVAGTNVMPGPNFS 889
```

RESULT 2

T18267

multidrug resistance protein - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18267

R;Shaulsky, G.; Kuspa, A.; Loomis, W.F.

submitted to the EMBL Data Library, January 1995

A:Description: An MDR transporter/serine protease gene is required for prestalk specialia;
A:Reference number: Z18850
A:Accession: T18267
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1905 <SHA>
A:Cross-references: UNIPROT:P54683; UNIPARC:UPI000013687C; EMBL:U20432; NID:g664839; PID
C:Genetics:
A:Gene: tagB

Query Match 22.1%; Score 497; DB 2; Length 1905;
Best Local Similarity 28.0%; Pred. No. 1.9e-23;
Matches 162; Conservative 72; Mismatches 162; Indels 182; Gaps 22;

```
Qy 19 LYGGQIIVAVADTGLDTCR---NDS-----SMHEAFRGKITALYALGRNTNANDTNGH 68
Dy 376 LRGGQILSIADTGLDGHCFSSKYPPIPNQVNNHNRKVT---YITHDNEDYVNGH 432
Qy 69 GTHVAGSVLGNG-----STNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSGAYSA 121
Dy 433 GTHVCGSAAGTPEDSSWAISSFGLATDAKIAFYD-LSSGSSEPTPEDYSQMYKPLYDA 491
Qy 122 GARIHTNSWGA---AVNGAYTTDSRNVDYVRK-NDMTILFAAGNEGPNGGTISAPGTA 176
Dy 492 GARVHGDGWSGVSLSQYVGYGSDDAGGIDAFLEYEPFESILRAAGN-NELFASLLAQATA 550
Qy 177 KNAITVGCATENLRPSFGS-----YADNI----- 199
Dy 551 KNAITVGAEQTAHVNVYVSDALEYYDFSDNANFORPCLFDKKYCNVTTAKCCSEVSNVKG 610
Qy 200 -----NHVAQFSRSGPTKDGRIKPDVMAFGTFILSARSS- 233
Dy 611 QLCCPASIKQNASDFTTQPFYNNENMGFSKGPETHDGLKPDIVAPGEYITSAKNG 670
Qy 234 -----LAPDSFWANHDSKIYMGTSMATPIVAGNVAQLRHF-----VKNRGI 278
Dy 671 ENSTDQCGDGL--PNANGLMSISGTSMATPLATAATTLIRQYLVGDGYPTGESVEENKL 728
Qy 279 TPKPSLLKAALIAAGADIGLY-----PNGNQGWGRVTLDKSLNVA 319
Dy 729 LPTGSLLKALMINNAQLNGTYFWSASSTPNPSNAIFEQINGANLIQGWALRMN---NWL 785
Qy 320 YVNESS-----SLSTSOKAT-----YSFT-----ATAGK 343
Dy 786 YVKSNTPTPSRWIGIGGLGKNQKATWKEDSLSSGLNKSICYTKPSSSSSGSGGGGT 845
Qy 344 P-LKISLWSDAPASTASVTLVNDLDL-----VITAPN-GTQYVGNDFTSFYND 391
Dy 846 PRIVATLVMTDPPSYGAKFNLVNLDLILLNSDDSDIITIGNSGGSLQPAKVAQP--- 902
Qy 392 NWDGRNVENVINAPQSGTYTIEVQAVNPVGPQTES 429
Dy 903 --DTLNNVEGIIINPTKAMNYKFTIAGTNVPIGPQKFS 938
```

RESULT 3

B83891

intracellular alkaline serine proteinase aprX [imported] - Bacillus halodurans (strain C)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: B83891

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: B83891

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-444 <STO>

A:Cross-references: UNIPROT:Q9KBJ7; UNIPARC:UPI000000C3D43; GB:AP001513; GB:BA000004; NID

A:Experimental source: strain C-125

C:Genetics:

A:Gene: aprX

Db 288 SGGTSGIPANPAEIVNMSLGGGSCSTTMQN-AINGAVSRGT-----TVV 334

Qy 158 PAAGNEGNCGTISAPGTAKNAITVGATEN--LRPSCGSYADNNHNHVAQFSSRGPTKDG 215

Db 335 VAAGNDASNVSG-SLPANCANVIAVAATTSAGAKASVNFGTGI----- 377

Qy 216 IKPDVMAPTGTFILSARSS--LAPDSSFANHDSKYAYMGGTSMATPIVAGNVAQLREHFV 273

Db 378 ---DVSAPGSSILSTLNSGTTTPGS-----ASYASVNGTSMASPHVAGVVALVQS--V 425

Qy 274 KNRGITPK--PSLKK--AALTAGAADIGLGYPNGNGQGRVTLKSLNVAVVNESS--- 325

Db 426 APTALTPAAVETLLKNVBARAPGAC-----SGCGGAGIWNADAAVTAA--INGSGGGG 477

Qy 326 -----SLTSOKATYSFTATAGKPLKISLWSDAPASTASVTL---VND 367

Db 478 GGGNTLNGTPTVGLGAATGAELNYTITVPAG-----SCTLTVTTSGSGSD 523

Qy 368 LDLVI---TAPNGTQYVGNDFTSYNDNWDGRNVNENFINAPOSGYTYTIEVQYVNVPG 424

Db 524 ADLYVRAGSAPTDASAYT---CRPYRS-----GNAETCTITAP-SGTYYVRLKAYS--- 569

Qy 425 PQTES 429

Db 570 --TFS 572

RESULT 8

S25835

subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain T441)

C;Species: Bacillus sp.

C;Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004

C;Accession: S25835

R;Davail, S.; Feller, G.; Narinx, E.; Gerday, C.

Gene 119, 143-144, 1992

A;Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacillus

A;Reference number: S25835; MUID:93012966; PMID:1398082

A;Accession: S25835

A;Molecule type: DNA

A;Residues: 1-419 <DAV>

A;Cross-references: UNIPARC:UPI00000BB77A; EMBL:X63533; NID:g40198; PID:CAA45096.1; PID

C;Superfamily: Subtilisin; subtilisin homology

C;Keywords: extracellular protein; hydrolase; serine proteinase

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-110/Domain: propeptide #status predicted <PRO>

F;111-419/Product: microbial serine proteinase #status predicted <MAT>

F;135-373/Domain: subtilisin homology <SBT>

F;144,184,359/Active site: Asp, His, Ser #status predicted

Query Match 12.5%; Score 281; DB 1; Length 419;

Best Local Similarity 33.0%; Pred. No. 1.3e-10;

Matches 87; Conservative 38; Mismatches 97; Indels 42; Gaps 13;

Qy 21 GQGQIVAVADTGLDTGRNDSNMH-EAPFGKITYALYALGRT---NNANDTNGHGHVAGSV 76

Db 135 GAGINIAVLDTGVNTNHPDLSNVVEQCKD-----FTVGTNFTDNCSTDRQGHGHVAGSA 189

Qy 77 LGNGSTNK---GMAPOANL-VFQSIMDSGGGLG-GLPSNLQTLFSQAYSAGARLHTN-SW 130

Db 190 LANGGTGSGVGVGAPEADLMAYKVLGDDGSGYADDIAEAIKRHAGDQATALNTKVVIMNSL 249

Qy 131 GAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEPGNGGTISAPGTAKNAITVGATENLRP 190

Db 250 GSSGESSILIT---NAV DYAYDKGVLLITAAAGNSGPKSGISGYPALYNAVAVALENTIQ 306

Qy 191 SFGSYADNINHVAQFSSRGPTKDG-----RIKPDVMAPTGTFILSARSSLAPDSSFWANH 244

Db 307 N-GTY-----RVADFSSRGHKRTAGDYVIQGDVEISAPGAAYVST-----W--F 348

Qy 245 DSKYAYMGGTSMATPIVAGNVAQL 268

Db 349 DGGYATISGTSMASPHVAGLAAKI 372

RESULT 9

G83753

subtilisin-type proteinase (EC 3.4.21.-) vpr precursor [similarity] - Bacillus haloduran

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: G83753

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: G83753

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-799 <STO>

A;Cross-references: UNIPROT:O9KEMI; UNIPARC:UPI00000C39DC; GB:AP001510; GB:BA000004; NID

A;Experimental source: strain C-125

C;Genetics:

A;Gene: vpr

C;Superfamily: microbial serine proteinase vpr; subtilisin homology

C;Keywords: hydrolase; serine proteinase

F;1-29/Domain: signal sequence #status predicted <SIG>

Query Match 12.5%; Score 280; DB 2; Length 799;

Best Local Similarity 24.7%; Pred. No. 3.7e-10;

Matches 117; Conservative 50; Mismatches 135; Indels 172; Gaps 16;

Qy 18 GLYCGQIVAVADTGLDTGRNDSMHEAPFGKITALYALGRTNNANDT-----NGH 68

Db 171 GYTGEGITVAILDTGVDTHTPD--LVHAF-GDYKGMDFIDNDDDPQETPGDPRGIETTH 227

Qy 69 GTHVAGSVLNGSTNKGMAPQANLVFOSIMDSGGGLGPSNLQTLFSQAYSAGARLHTN 128

Db 228 GTHVAGTVAANGLI-KGVAPEANLLAVRVLPGG--RGSTAGVIAGIERAVQDGADIMNL 284

Qy 129 SWGAANVAVTDSRVNDDYVRKNDMTILFAAGNEPGNGGTISAPGTAKNAITVGATENL 188

Db 285 SLGNTLNDPDPFATSIAL-DWMAEGVAVTSSNGSNPNWTVGSPGTSRDAISVGAT--- 340

Qy 189 RPSFGSV-----ADINIH----- 201

Db 341 RLPYNTKASVFTSDGIDYPSADIMGFPDSDEELLELDGETYEYAFAGLKGPGDFEGVDVE 400

Qy 202 ----- 201

Db 401 GKIALIVRGIPFVEXAENAKAGAVCAIIYNNVAGVQTPVPGIAIPTIMLSNEDGLKMR 460

Qy 202 -----VAQFSSRGPT-KDGRIKPDVMAPTGTFILSARSSLAPD 237

Db 461 NELENGQNTVTFSTIEFDPKLVGETVADFSRGRPVNHTWMIKPDVSPAGVAIVSTIPTHPD 520

Qy 238 SSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALTAGRADI- 296

Db 521 DPY-----GYGRQGTSMASPHVAGAAALLLEAH-PNWGV----DHVKAALMNTAENLV 569

Qy 297 ---GLGYPNGNGQGRVTLDKSLNVAVVNESSLSSTSQATY-SFTATAGKPLK 346

Db 570 DENGNYPHNTQAG-----SIRIVDAIESETLVTPGSHSGFTFKERKQVE 617

RESULT 10

T29090

surface layer-associated STABLE proteinase - Staphylothermus marinus

N;Alternate names: hyperthermostable proteinase

C;Species: Staphylothermus marinus

C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C;Accession: T29090

R;Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.

Curr. Biol. 6, 739-749, 1996

A;Title: A hyperthermostable protease of the subtilisin family bound to the surface layer

A;Reference number: Z20559; MUID:96385442; PMID:8793300

A;Accession: T29090

A;Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA
 A:Residues: 1-1345 <MAT>
 A:Cross-references: UNIPROT:Q54437; UNIPARC:UPI0000062778; EMBL:U57968; NID:gl374755; PIDN
 A:Experimental source: strain F1
 C:Function:
 A:Description: probably serves an exodigestive function related to the organism's energy
 A:Note: stoichiometric 8-layer component

Query Match 12.4%; Score 279.5; DB 2; Length 1345;
 Best Local Similarity 29.9%; Pred. No. 7.9e-10;
 Matches 99; Conservative 45; Mismatches 106; Indels 81; Gaps 14;

QY 46 PRGKITALYALGRNTNANDTNGHGTVA-----GSLV-----GNGSTNK--GMAPOANLV 93
 DB 445 YQGRYLAL-----VSDFHGHTSVNTVTSRGRVLYDYGDKLYRMGVAPGAKI- 495
 QY 94 PQSIMDSGGGLGLPSNLQTLFSQAYSAG-----AARIHTNSW 130
 DB 496 -----AGGDALLGNLVL--EAWLAGFNIVTEEDGVYVLSLDPPGPHRADIIISNW 546
 QY 131 GAAVNGAYTTDSRNV-----DYVRKNDMTILFAAGNEGPNGGTISAPGTAK 177
 DB 547 GSIWFLWQFPGLDYSRSEFMDEILAIRNYLIGDHVTIVFAAGNEGPGYSSNGAPGTGL 606
 QY 178 NAITVGATE--NLRPSFG---SYADNINHVAQFSRGTGDKRIKPDVMAPTGTFILSARS 232
 DB 607 LVITAGASTLDYTRIYGYPEGYAD---EVIPIFSRGTGQGYPKPDIVNIGAFEMASTR 663
 QY 233 SLAPDSSFWANHDSKYAVMGTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAAALIAAG 292
 DB 664 TI-DORGGAQPD---VFGTSEATPYTSGTLALVFQAYKEVYNTTDPDPTAKIILKSS 718
 QY 293 AADIGLVPNGQNGRVTLDKSLNAVYNE 323
 DB 719 AKDI--WYPAFSQSGRVDALKAADTVPISE 747

RESULT 11
 S23407
 Subtilisin (EC 3.4.21.62) 1 precursor - Bacillus sp. (strain TA39)
 C:Species: Bacillus sp.
 C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004
 C:Accession: S23407
 R:Narinx, E.; Davail, S.; Feller, G.; Gerday, C.
 Biochim. Biophys. Acta 1131, 111-113, 1992
 A:Title: Nucleotide and derived amino acid sequence of the subtilisin from the antarctic
 A:Reference number: S23407; MUID:92256481; PMID:1581352
 A:Accession: S23407
 A:Molecule type: DNA
 A:Residues: 1-420 <NAR>
 A:Cross-references: UNIPROT:P28842; UNIPARC:UPI0000136183; EMBL:X62369; NID:g40200; PIDN
 C:Genetics:
 A:Gene: sub1
 C:Superfamily: Subtilisin; subtilisin homology
 C:Keywords: extracellular protein; hydrolase; serine proteinase
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-111/Domain: propeptide #status predicted <PRO>
 F:112-420/Product: microbial serine proteinase #status predicted <MAT>
 F:136-374/Domain: subtilisin homology <SBT>
 F:145,185,360/Active site: Asp, His, Ser #status predicted

Query Match 12.3%; Score 277; DB 1; Length 420;
 Best Local Similarity 31.2%; Pred. No. 2.4e-10;
 Matches 98; Conservative 44; Mismatches 120; Indels 52; Gaps 16;

QY 21 GOGQIVAVADTGLDGTGRNDSMHEAFRGKITAL--VALGRT---NANDTNGHGTVAAGS 75
 DB 136 GGGINIAVLDTGVNTN-----HPDLRNVECKQFTVGTNTNSCTDRQGHGTVAAGS 189
 QY 76 VLNGSTNK--GMAPOANL--VFQSIMDSGGGLG--GLPSNLOTFLSQAYSAGARIHTN-S 129
 DB 190 ALADGGTGVGVAPDADLWAYKVLGDGSGYADIAAAIRHAGDQAATLNTKVVINMS 249

QY 130 WGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAITVGATENLR 189
 DB 250 LGSSESSLITNAV---YSYNGVLLIIAAGNSGYPQSGISGYPGALVNAVAALLEN-K 305
 QY 190 PSFGSYADNINHVAQFSRGTG-KDG-----RIKPDVMAPTGTFILSARSLAPDSSFWAN 243
 DB 306 VENGTY-----RVADFSRSGYSTGDIATQKQDVEISAPGAAYST-----W--- 348
 QY 244 HDSKYAVMGTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAAALIAAGADIGLGPNG 303
 DB 349 FDGGYATISGTSWASPHRAAGLAAKIWAQYPSASNVVRGELQYRAY---ENDILSGIYAG 405
 QY 304 -----NQGMGRVTL 312
 DB 406 YGDDFASGFGFATV 419

RESULT 12
 JC4908
 alkaline serine proteinase (EC 3.4.-.-) I precursor - Alteromonas sp.
 N:Alternate names: sutilsase
 C:Species: Alteromonas sp.
 C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 05-Oct-2004
 C:Accession: JC4908
 R:Tsujiibo, H.; Miyamoto, K.; Tanaka, K.; Kaidzu, Y.; Imada, C.; Okami, Y.; Inamori, Y.
 Biosci. Biotechnol. Biochem. 60, 1284-1288, 1996
 A:Title: Cloning and sequence analysis of a protease-encoding gene from the marine bacter
 A:Reference number: JC4908; MUID:97141200; PMID:8987544
 A:Accession: JC4908
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-715 <TSU>
 A:Cross-references: UNIPROT:P70765; UNIPARC:UPI000017A928; DBJ:D38600; NID:gl536787; PII
 A:Experimental source: strain O-7
 C:Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sensit
 C:Genetics:
 A:Gene: aprI
 C:Superfamily: extracellular alkaline serine protease precursor, Alteromonas type
 C:Keywords: hydrolase
 F:1-40/Domain: signal sequence #status predicted <SIG>
 F:41-150/Domain: amino-terminal propeptide #status predicted <ATP>
 F:151-496/Product: alkaline serine protease I #status predicted <MAT>
 F:182-452/Domain: subtilisin homology <SBT>
 F:497-715/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F:239-294,335-372,478-481/Disulfide bonds: #status predicted

Query Match 11.9%; Score 267; DB 2; Length 715;
 Best Local Similarity 25.9%; Pred. No. 2.1e-09;
 Matches 124; Conservative 51; Mismatches 168; Indels 136; Gaps 23;

QY 21 GOGQIVAVADTG-----LDTGRNDSMHEAFRGKITALYALGRTNNAND-----TNG----- 67
 DB 182 GQGVVAVLDTGYRPHLDLDANILPGYDMISNTFVANDGGARDNDARDPGDAVTRGEGCT 241
 QY 68 -----HGTHVAG---SVLGNSTNGKMAPQANLVFOSIMDSGGGLGLP 108
 DB 242 DSSGQVPVPRADQSSWHGTHVAGTVAATNNGEGVAGVAYDAKVVPVRL---GKCGGLT 298
 QY 109 SNLQTLFSQAYSAGARIHTNSWGAIV-----NGAYTTDSRNVDDYVRKNDMTILFAAG 161
 DB 299 SDIADGIIWASGGSDRVPAANPAVIVNWSLGGGACSAATTQNAINQARNNGTIVIAAG 358
 QY 162 NEGPNGGTISAPGTAKNAITVGAT--ENLRPSFGSYADNINHVAQFSRGTGDKRIKPD 219
 DB 359 NDNDNSANYN--PGNCNGVNVVASVGRGSRAYSYNGANI-----D 398
 QY 220 VMAPGTFTLSARSLAPDSSFWANHDS-----KYAYMGTSMATPIVAGNVAQLR-- 269
 DB 399 VAAFG-----GAQSPADDPGEGILSTHNSGAPSNDSYHSQGSTWAAPHVAGVAALIKQA 454
 QY 270 -----EHFVKV--RGITPKPSLLKAAALIAAGADI--GLG-----YPNGNQGHGRVTL 312
 DB 455 KPSATPDEVEITLKNTRSFAGSCSNCGTGVVDAAAANEAALGDVVVTPPTGTN-----TL 508

A72647
Probable surface layer-associated STABLE proteinase APE0607 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A72647
C:Author: A. Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kato, Y.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: A72647
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1331 <XAW>
A:Cross-references: UNIPROT:Q9VEG9; UNIPARC:UPI000005DBF6; DBJ:AP000060; NID:G5104188;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0607

	Query Match	11.7%; Score 263; DB 2; Length 1331;
	Best Local Similarity	23.6%; Pred. No. 8.8e-09;
	Matches 111; Conservative	65; Mismatches 158; Indels 136; Gaps 18;
Qy	8 VKADVAOSSYGLYGOGIIVAVADTGLDTRNDSSMHE-AFRGKITALYA-----	55
Dd	346 VYADLS-TAYLYF-----LKALSDTGMTSGPDSPLDLLDSPADETAPSYSGEVLARDFTGD	400
Qy	56 -----LGTNNAN-----	DTNGH 68
Dd	401 GVNDFSAGALAGWTYDWVGLLTGBESVNLGRWLGFDYAGLVLPGLDPQRWVSILYDTLAH	460
Qy	69 GTHVAGSVLGNGSIN-----KGMAQANILVFQSIMDSGGGLGGLPSNQLTFSQLA	118
Dd	461 GTSVATVIASRGNVFEWNLGIETSLRGAVPACAKIA-----AGGSF-----LINVFVAQL	509
Qy	119 YSAG-----ARIHTNSWG--AAVNGAVT--TDSRNVDYD-VRKNDMT	155
Dd	510 FLSCGFEDQPDLNWVYTGEHQVDVINNSWGNYSIALRGFLTGADDYATIEDIYVSASGV	569
Qy	156 ILFAAGNEGNGGTTISAPGTAKNAITVGATE--NLRFSPGSIADNINHVAQFSRGPTKD	213
Dd	570 IVHAMGNGGPGCYGATTTPGAGSLTIISVGASTLFDIRPFYGYLPSPGGDVTSWDRGPSQI	629
Qy	214 GRIPDYMACTFTLSARSSLAPDSSFWANHDSKYAYMGCTSMATPIVAGNVAQLREHFV	273
Dd	630 GVAKPDVVNTIGSFAWAG----VPVLTLGLNGSLAFIDFGGTSEATPMTSGVALVISAYQ	685
Qy	274 KNRGITPKPSLLKAALTAGAADIGLGPNGQGMRVTLDKSLN-----AY	320
Dd	686 QAFCAKSPGLVKAILKSTARDTGA--DAFTQSGQDVVYRAVKAVLEGGVPIALSTSIVY	743
Qy	321 VNNESSISTOKATYSTATAGKPKLKSILWSDSA--PASTTASVTLVNDL	368
Dd	744 ENVYSLLS-----GYSYPFLAPNPVEDTQIYPGLVKPGETAVENTLVKLKTLL	788

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Qy 274 KNRGITPKPSLLKAALTAGADIGLPGNQGWRVTLDKSLNV-----AY 320
Db 686 QAFGAKPSPGLVAILKSTARDTGA--DAFTQSGQVDVYRAVKAVLGGVPIALSTSVY 743
Qy 321 VNESSSLSSTQKATYSFTATAGKPKLISLVWSDA--PASTTASVTLVNDL 368
Db 744 ENVYSLLS-----GYSYFFLAPNPVEDTQIYPGVLKPGETA VETLVLKTL 788

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RESULT 14

C84120

subtilisin-type proteinase (EC 3.4.21.-) BH3763 precursor [similarity] - Bacillus halodurans

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: C84120

A; Cross-references: UNIPROT:P08594; UNIPARC:UPI0000125DOA; GB:D90108; GB:J05444; GB:J05445; GB:J05446; GB:J05447; GB:J05448; GB:J05449; GB:J05450; GB:J05451; GB:J05452; GB:J05453; GB:J05454; GB:J05455; GB:J05456; GB:J05457; GB:J05458; GB:J05459; GB:J05460; GB:J05461; GB:J05462; GB:J05463; GB:J05464; GB:J05465; GB:J05466; GB:J05467; GB:J05468; GB:J05469; GB:J05470; GB:J05471; GB:J05472; GB:J05473; GB:J05474; GB:J05475; GB:J05476; GB:J05477; GB:J05478; GB:J05479; GB:J05480; GB:J05481; GB:J05482; GB:J05483; GB:J05484; GB:J05485; GB:J05486; GB:J05487; GB:J05488; GB:J05489; GB:J05490; GB:J05491; GB:J05492; GB:J05493; GB:J05494; GB:J05495; GB:J05496; GB:J05497; GB:J05498; GB:J05499; GB:J05500; GB:J05501; GB:J05502; GB:J05503; GB:J05504; GB:J05505; GB:J05506; GB:J05507; GB:J05508; GB:J05509; GB:J05510; GB:J05511; GB:J05512; GB:J05513; GB:J05514; GB:J05515; GB:J05516; GB:J05517; GB:J05518; GB:J05519; GB:J05520; GB:J05521; GB:J05522; GB:J05523; GB:J05524; GB:J05525; GB:J05526; GB:J05527; GB:J05528; 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GB:J05893; GB:J058

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Eur. J. Biochem. 173, 491-497, 1988
A:Title: Nucleotide sequence of the gene for aqualysin I (a thermophilic alkaline serine
A:Reference number: S00620; MUID:8225062; PMID:3286255
A:Accession: S00620
A:Molecule type: DNA
A:Residues: 75-442 <KWO>
A:Cross-references: UNIPARC:UPI0000170448; EMBL:X07734; NID:948069; PIDN:CAA30559.1; PID
A:Note: part of this sequence, including the amino and carboxyl ends of the mature prote
R:Matsumura, H.; Tokugawa, K.; Hamaki, M.; Mizoguchi, H.; Terada, I.; Kwon
Eur. J. Biochem. 171, 441-447, 1988
A:Title: Purification and characterization of aqualysin I (a thermophilic alkaline serin
A:Reference number: S00324; MUID:88151937; PMID:3162211
A:Accession: S00324
A:Molecule type: protein
A:Residues: 128-170 <MATS>
A:Cross-references: UNIPARC:UPI0000172C23
C:Superfamily: Subtilisin; subtilisin homology
C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-14/Domain: signal sequence #status predicted <SIG>
F:15-127/Domain: propeptide #status predicted <PRO>
F:128-408/Product: aqualysin I #status experimental <MAT>
F:157-364/Domain: subtilisin homology <SBT>
F:255-257,281-283/Region: S1 specificity crevice #status predicted
F:409-513/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F:166,197,349/Active site: Asp, His, Ser #status predicted

Query Match      11.5%; Score 257.5; DB 1; Length 513;
Best Local Similarity 26.0%; Pred. No. 5.4e-09;
Matches 117; Conservative 44; Mismatches 144; Indels 145; Gaps 23;

QY      16 SYGLYGGOIIVAVADTGLDGTGRNDSSMHEAPRGKITALLY-ALGRTNNANDTNGHGHVAG 74
Db      152 TYTATGRGVNVYIDTIGRT-----THREPGGARVGVYDALG--GNGQDCNCGHGHVAG 203

QY      75 SVLGNSTNKGMAPQANLVFQSIIMD--SGGGLGGLPSNLQTLFSQAYSAGARIHTN---- 128
Db      204 TI---GGVTYGVAKAVNLVAVRLDCNGSGSTSGVIAGVDWV-----TRNHRPPAVA 252

QY      129 ---SWGAAVNGAYTTDSRVDDYVRKN-----DMTILFAAGNEGPNGGTISAPGTAKNAITVG 183
Db      253 NMSLGGGVSTA-----LDNAVKNSTAAAGVYVAAAGNDNANACNYS-PARVAEALTVG 304

QY      184 AT--ENLRPSFGSYADNINHVAFQSSRGPTKDGRIKPDVMAPTGFIILSARSLAPDSSF 241
Db      305 ATSSDARAFSNVGSV-----DLFAPGASIPSA-----W 335

QY      242 ANHDSKYAYMGSTMATPIVAGNVAQLREHFVKNRGITP---KPSLLKAALIAGAADIGL 298
Db      336 YTSDTATQTTLNGTSMATPHVAG-VAAL--YLEQNPSATPASVASAILNGATTGRLSGIGS 392

QY      299 GYPNGNQGWGRVTLDKSLNAVYVNESSLSLTSQKATYSFTATAGKPLKISLVNSDAPAST 358
Db      393 GSPN-----RLLYSLLSSGS-----GSTAPCTS 415

QY      359 ---TASVTLVNDLDELVTAPNGTQY-----VGNDFTSPYNDNDGDN--- 397
Db      416 CSYITGSLSGGPDYNF---QNGTYIYSPAGTHRAWLKGPA GTDF-DLYLWRWDGSRWLT 471

QY      398 -----NVENVFINAPQSGTYTIEVQAYN 420
Db      472 VGSSTGPTSEESLSYSGTAGYVYLWRIYAYS 501

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Search completed: March 30, 2006, 08:33:55
Job time : 44 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2006, 08:26:16 ; Search time 228 Seconds
(without alignments)
1342.979 Million cell updates/sec

Title: US-10-820-712A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSGLY.....EVOAYNPVGPQTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2247	100.0	640	2 Q93UV9_9BACI	Q93UV9 bacillus sp
2	2242	99.8	640	2 Q76184_9BACI	Q76184 bacillus sp
3	2183	97.2	639	2 Q9AQR3_9BACI	Q9AQR3 bacillus sp
4	2143	95.4	434	2 Q9AQR0_9BACI	Q9AQR0 bacillus sp
5	1998.5	88.9	433	2 Q9AQR1_9BACI	Q9AQR1 bacillus sp
6	1994.5	88.8	433	2 Q9AQR4_9BACI	Q9AQR4 bacillus sp
7	1987.5	88.5	433	2 Q9AQR2_9BACI	Q9AQR2 bacillus sp
8	870.5	38.7	697	2 Q4NB18_9M1CC	Q4NB18 arthrobacte
9	754.5	33.6	711	2 Q6MKR4_BDEBA	Q6MKR4 bdellovibri
10	739.5	32.9	1748	2 Q4NVB5_GDELT	Q4NVB5 anaeromyxob
11	592	26.3	1088	2 Q4HUV5_GIBZE	Q4HUV5 giberella
12	580	25.8	2030	2 Q747P6_GEOSL	Q747P6 geobacter s
13	531.5	23.7	1741	2 Q54M84_DICDI	Q54M84 dictyosteli
14	523.5	23.3	1743	1 TAGC_DICDI	Q23868 dictyosteli
15	511.5	22.8	1825	2 Q8T9W1_DICDI	Q8T9W1 dictyosteli
16	497	22.1	1905	1 TAGB_DICDI	Q54683 dictyosteli
17	497	22.1	1906	2 Q54M83_DICDI	Q54M83 dictyosteli
18	447	19.9	1752	2 Q9GNT7_DICDI	Q9GNT7 dictyosteli
19	425.5	18.9	1388	2 Q580U9_9TRYP	Q580U9 trypanosoma
20	414	18.4	654	2 Q8UOC9_PYRFU	Q8UOC9 pyrococcus
21	414	18.4	663	2 Q5J1Z5_PYRKO	Q5J1Z5 pyrococcus
22	406.5	18.1	561	2 Q8RBJ2_THETN	Q8RBJ2 thermoanaer
23	398	17.7	1239	2 Q9FBZ4_STRCO	Q9FBZ4 streptomyc
24	381	17.0	430	2 Q8ENV1_OCEIH	Q8ENV1 oceanobacil
25	376	16.7	1253	2 Q9FCO6_STRCO	Q9FCO6 streptomyc
26	366	16.3	1102	2 P95684_STRAC	P95684 streptomyc
27	363.5	16.2	1208	2 Q82BI4_STRAW	Q82BI4 streptomyc
28	349	15.5	1245	2 Q9RL54_STRCO	Q9RL54 streptomyc
29	347.5	15.5	444	2 Q9KBJ7_BACHD	Q9KBJ7 bacillus ha
30	346.5	15.4	1139	2 Q82I39_STRAW	Q82I39 streptomyc
31	346	15.4	1105	2 Q8KKH6_STRVD	Q8KKH6 streptomyc

32	340	15.1	442	2 Q5L315_GEOKA	Q5L315 geobacillus
33	338	15.0	412	2 Q9AER6_THEYO	Q9AER6 thermoanaer
34	338	15.0	1237	2 Q8GQT4_STRAZ	Q8GQT4 streptomyc
35	337	15.0	412	2 Q8RC68_THETN	Q8RC68 thermoanaer
36	337	15.0	1294	2 Q50HM7_STRSH	Q50HM7 streptomyc
37	336	15.0	795	2 Q5NW24_9ARCH	Q5NW24 uncultured
38	332.5	14.8	442	2 Q651P4_BACLD	Q651P4 bacillus li
39	328.5	14.6	1220	2 Q91LOA0_STRCO	Q91LOA0 streptomyc
40	327.5	14.6	435	2 Q8EMJ3_OCEIH	Q8EMJ3 oceanobacil
41	324.5	14.4	818	2 Q79CG2_BACSP	Q79CG2 bacillus sp
42	324.5	14.4	824	2 Q45464_BACSP	Q45464 bacillus sp
43	320.5	14.3	442	2 Q31788_BACSU	Q31788 bacillus su
44	320.5	14.3	891	2 Q93635_THESU	Q93635 thermococcu
45	310.5	13.8	806	1 SUBV_BACSU	P29141 bacillus su
46	308.5	13.7	431	2 Q9S3L6_BACSH	Q9S3L6 symbiobacte
47	308	13.7	1899	2 Q67RJ0_SYMTH	Q67RJ0 bacillus su
48	307.5	13.7	646	2 Q5Z876_BACSU	Q5Z876 bacillus su
49	306.5	13.6	524	2 Q5UEH9_PYRKO	Q5UEH9 pyrococcus
50	306.5	13.6	1398	2 Q9P9L1_PYRMO	Q9P9L1 pyrococcus
51	304.5	13.6	1398	1 PLS_PYRFU	P72186 pyrococcus
52	297	13.2	1135	2 Q9P9D1_9EURY	Q9P9D1 uncultured
53	294.5	13.1	434	2 Q54327_BACSH	Q54327 bacillus sp
54	290	12.9	891	2 Q4H8C2_9DEIO	Q4H8C2 deinococcus
55	289	12.9	798	2 Q68YD0_9BACI	Q68YD0 bacillus sp
56	288.5	12.8	808	2 Q6L9U6_9BACI	Q6L9U6 bacillus sp
57	287.5	12.8	798	2 Q68YD2_9BACI	Q68YD2 bacillus sp
58	286.5	12.8	802	2 Q65DN2_BACLD	Q65DN2 bacillus li
59	286	12.7	848	2 Q4HCE6_9DEIO	Q4HCE6 deinococcus
60	285.5	12.7	808	2 Q6L9U7_9BACI	Q6L9U7 bacillus sp
61	285	12.7	808	2 Q6X5Y8_XANNA	Q6X5Y8 xanthomonas
62	285	12.7	798	2 Q68YD1_9BACI	Q68YD1 bacillus sp
63	283	12.6	416	2 Q6W4N2_9BACI	Q6W4N2 bacillus sp
64	283	12.6	580	1 EXPR_XANCP	P23314 xanthomonas
65	283	12.6	580	2 Q4URAO_XANCP	Q4URAO xanthomonas
66	282.5	12.6	586	2 Q4UT02_XANCP	Q4UT02 xanthomonas
67	282.5	12.6	586	2 Q8PAL8_XANCP	Q8PAL8 xanthomonas
68	282.5	12.6	807	2 Q6L9U5_9BACI	Q6L9U5 bacillus sp
69	281	12.5	419	2 Q45681_BACSU	Q45681 bacillus su
70	280.5	12.5	514	2 Q4H6A0_9DEIO	Q4H6A0 deinococcus
71	280.5	12.5	808	2 Q6L9U8_9BACI	Q6L9U8 bacillus sp
72	280	12.5	799	2 Q9KEM1_BACHD	Q9KEM1 bacillus ha
73	279.5	12.4	1345	2 Q54437_STAWA	Q54437 staphylothe
74	278.5	12.4	959	2 Q8PMS7_XANAC	Q8PMS7 xanthomonas
75	277.5	12.3	621	2 Q9F486_ALTSO	Q9F486 alteromonas
76	277.5	12.3	621	2 Q53401_9ALTE	Q53401 alteromonas
77	277.5	12.3	1467	2 Q4W8M2_9BACI	Q4W8M2 bacillus sp
78	277	12.3	420	1 SUBT_BACS9	P28842 bacillus sp
79	277	12.3	942	2 Q5HIN5_XANOR	Q5HIN5 xanthomonas
80	273.5	12.2	513	2 Q64FJ8_9DEIN	Q64FJ8 thermus sp.
81	272.5	12.1	568	2 Q8PMC0_XANAC	Q8PMC0 xanthomonas
82	272.5	12.1	575	2 Q8PNW1_XANAC	Q8PNW1 xanthomonas
83	271.5	12.1	759	2 Q5WB69_BACSK	Q5WB69 bacillus cl
84	270	12.1	1101	2 Q82CF0_STRAW	Q82CF0 streptomyc
85	268.5	11.9	403	2 Q45463_BACSP	Q45463 bacillus sp
86	268.5	11.9	814	2 Q82VB3_NITEU	Q82VB3 nitrosomona
87	267.5	11.9	1413	2 Q4VN43_BACEE	Q4VN43 bacillus ce
88	267	11.9	715	2 P70765_ALTSO	P70765 alteromonas
89	265	11.8	1098	2 Q6L1Z8_STRCO	Q6L1Z8 streptomyc
90	265	11.8	1406	2 Q632G9_BACZZ	Q632G9 bacillus ce
91	265	11.8	1627	2 Q5F1Z3_LACAC	Q5F1Z3 lactobacill
92	264.5	11.8	966	2 Q4US13_XANCP	Q4US13 xanthomonas
93	264.5	11.8	966	2 Q8PB28_XANCP	Q8PB28 xanthomonas
94	263	11.7	701	2 Q84FM9_FERIS	Q84FM9 fervidobact
95	263	11.7	1331	2 Q9YEG9_AERPE	Q9YEG9 aeropyrum p
96	263	11.7	1571	2 Q8GCW3_STRAG	Q8GCW3 streptococc
97	262.5	11.7	617	2 Q93IQ4_XANNA	Q93IQ4 xanthomonas
98	262.5	11.7	1407	2 Q4MN80_BACCE	Q4MN80 bacillus ce
99	262	11.7	1407	2 Q816G4_BACCR	Q816G4 bacillus ce
100	261	11.6	425	2 Q647R6_9ARCH	Q647R6 uncultured

ALIGNMENTS

RESULT 1

Q93UV9_9BACI
 ID Q93UV9_9BACI PRELIMINARY; PRT; 640 AA.
 AC Q93UV9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Protease.
 GN Name=PROF;
 OS Bacillus sp. KSM-KP43.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=109322;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=KP43;
 RA Itoh S., Saeki K.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB051423; BAB55674.2; -; Genomic_DNA.
 DR PDB; 1WMD; X-ray; A=207-640.
 DR PDB; 1WME; X-ray; A=207-640.
 DR PDB; 1WMF; X-ray; A=207-640.
 DR MEROPS; S08.123; -.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR007280; Pept_Bact_C.
 DR Pfam; PF00082; Pept_S8_S53.
 DR Pfam; PF04151; PPC; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 640 AA; 67991 MW; 4BBAF77E9D592C15 CRC64;

Query Match 100.08; Score 2247; DB 2; Length 640;
 Best Local Similarity 100.08; Pred. No. 4.2e-139; Indels 0; Gaps 0;
 Matches 434; Conservative 0; Mismatches 0;
 QY 1 NDVARGIVKADVAGSSYGLYGQGI VAVADTGLDTGRNDSMHFAFRGKITALYALGRTN 60
 DB 207 NDVARGIVKADVAGSSYGLYGQGI VAVADTGLDTGRNDSMHFAFRGKITALYALGRTN 266
 QY 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
 DB 267 NANDTNGHGTHTVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
 QY 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
 QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 240
 DB 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 446
 QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 300
 DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 506
 QY 301 PNGNGWGRVTLDKSLNAVYNESSLSSTSKATYSFTATAGPKPKISLVMSDAPASTTA 360
 DB 507 PNGNGWGRVTLDKSLNAVYNESSLSSTSKATYSFTATAGPKPKISLVMSDAPASTTA 566
 QY 361 SVTLVNDLDELVTAPNGTQYVGNDFTPSYNDNWDGRNNVENVFVINAPOSQTYTIEVQAYN 420
 DB 567 SVTLVNDLDELVTAPNGTQYVGNDFTPSYNDNWDGRNNVENVFVINAPOSQTYTIEVQAYN 626
 QY 421 VPVGPQTFSLAIVN 434
 DB 627 VPVGPQTFSLAIVN 640

RESULT 3
 Q9AQR3_9BACI
 ID Q9AQR3_9BACI PRELIMINARY; PRT; 639 AA.
 AC Q9AQR3;

RESULT 2

Q76L84_9BACI
 ID Q76L84_9BACI PRELIMINARY; PRT; 640 AA.
 AC Q76L84;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Protease.
 OS Bacillus sp. KSM-9865.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=192495;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=KSM-9865;
 RA Okuda M., Saeki K., Kobayashi T.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB084155; BAC82522.1; -; Genomic_DNA.
 DR HSSP; P00782; IAQN.
 DR SMR; Q76L84; 207-640.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR007280; Pept_Bact_C.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR Pfam; PF04151; PPC; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 640 AA; 67940 MW; 421F7A150FF2868F CRC64;

Query Match 99.88; Score 2242; DB 2; Length 640;
 Best Local Similarity 99.88; Pred. No. 9e-139; Indels 0; Gaps 0;
 Matches 433; Conservative 1; Mismatches 0;
 QY 1 NDVARGIVKADVAGSSYGLYGQGI VAVADTGLDTGRNDSMHFAFRGKITALYALGRTN 60
 DB 207 NDVARGIVKADVAGSSYGLYGQGI VAVADTGLDTGRNDSMHFAFRGKITALYALGRTN 266
 QY 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
 DB 267 NANDTNGHGTHTVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
 QY 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
 QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 240
 DB 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 446
 QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 300
 DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 506
 QY 301 PNGNGWGRVTLDKSLNAVYNESSLSSTSKATYSFTATAGPKPKISLVMSDAPASTTA 360
 DB 507 PNGNGWGRVTLDKSLNAVYNESSLSSTSKATYSFTATAGPKPKISLVMSDAPASTTA 566
 QY 361 SVTLVNDLDELVTAPNGTQYVGNDFTPSYNDNWDGRNNVENVFVINAPOSQTYTIEVQAYN 420
 DB 567 SVTLVNDLDELVTAPNGTQYVGNDFTPSYNDNWDGRNNVENVFVINAPOSQTYTIEVQAYN 626
 QY 421 VPVGPQTFSLAIVN 434
 DB 627 VPVGPQTFSLAIVN 640

RESULT 3
 Q9AQR3_9BACI
 ID Q9AQR3_9BACI PRELIMINARY; PRT; 639 AA.
 AC Q9AQR3;

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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Name=PROA;
GN Name=PROA;
OS Bacillus sp. 9860.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133778;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9860;
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046403; BAB21266.2; -; Genomic_DNA.
DR HSSP; P00782; 1SUP.
DR SMR; Q9AQR3; 206-639.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:proteolysis and peptidolysis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 639 AA; 68186 MW; 316AF6FFDBE4FF54 CRC64;

Query Match 97.2%; Score 2183; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 6.7e-135;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAAQSSYGLYGQGOIVAVADTGLDTGRNDSMHEAFRGKITALVALGRTN 60
Db 206 NDVARGIVKADVAAQSSYGLYGQGOIVAVADTGLDTGRNDSMHEAFRGKITALVALGRTN 265

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 266 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 325

Qy 121 AGARIHTNSWGAAYNGAYTTDSRVVDYVRKNDMTILFAAGNEPNGGTTISAPGTAKNAI 180
Db 326 AGARIHTNSWGAAYNGAYTTDSRVVDYVRKNDMTILFAAGNERPNGGTTISAPGTAKNAI 385

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPCGTFILSRSSILAPDSSF 240
Db 386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPCGTFILSRSSILAPDSSF 445

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLY 300
Db 446 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLY 505

Qy 301 PNGQGWGRVTLDKSLNVAAYVNESSISTSKATYFTATAGKPLKISLWSDAPASTTA 360
Db 506 PNGQGWGRVTLDKSLNVAAYVNESSISTSKATYFTATAGKPLKISLWSDAPASTTA 565

Qy 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 566 SVTLVNDLVLITAPNGTRYVGNDFSPAFDNNWDGRNNVENVFINPQSGTYTIEVOAYN 625

Qy 421 VPVGQPTFSLAIVN 434
Db 626 VPVGQPTFSLAIVN 639

Query Match 95.4%; Score 2143; DB 2; Length 434;
Best Local Similarity 93.5%; Pred. No. 1.7e-132;
Matches 406; Conservative 19; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAAQSSYGLYGQGOIVAVADTGLDTGRNDSMHEAFRGKITALVALGRTN 60
Db 1 NDVARGIVKADVAAQSSYGLYGQGOIVAVADTGLDTGRNDSMHEAFRGKITALVALGRTN 60

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120

Qy 121 AGARIHTNSWGAAYNGAYTTDSRVVDYVRKNDMTILFAAGNEPNGGTTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAYNGAYTTDSRVVDYVRKNDMTILFAAGNEPNGGTTISAPGTAKNAI 180

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPCGTFILSRSSILAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPCGTFILSRSSILAPDSSF 240

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLY 300

Qy 301 PNGQGWGRVTLDKSLNVAAYVNESSISTSKATYFTATAGKPLKISLWSDAPASTTA 360
Db 301 PNGQGWGRVTLDKSLNVAAYVNESSISTSKATYFTATAGKPLKISLWSDAPASTTA 360

Qy 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTKYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 420

Qy 421 VPVGQPTFSLAIVN 434
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Db 421 VPGQPAFSLAIVN 434
|| ||| |||||
360 SYTLVNDLDLVITAPNGQKVGNDFFPYDNDWGRNNVENFINAPQSGTYTIEVQAYN 419

RESULT 5
Q9AQR1_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROD;
OS Bacillus sp. SD521.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133780;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SD521;
RX MEDLINE=20568675; PubMed=1118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046405; BAB21268.1; -; Genomic_DNA.
DR HSSP; Q45670; 1DBI.
DR SMR; Q9AQR1; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolyase; Protease; Serine protease.
FT NON_TER 1
FT NON_TER 433
SQ SEQUENCE 433 AA; 45576 MW; 98A2DF18FE66DDC CRC64;

Query Match 88.9%; Score 1998.5; DB 2; Length 433;
Best Local Similarity 87.8%; Pred. No. 5.2e-123;
Matches 381; Conservative 28; Mismatches 24; Indels 1; Gaps 1;

QY 1 NDVARGIVKADVAAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
Db 1 NDVARGIVKADVAAQNYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60

QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 61 NANDPNGHGHVAGSVLGN-ALNKGMAPOANLVFQSIMDSGGGLGGLPSNLTLFQAWN 119

QY 121 AGARIHTNSGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGTISAPGTAKNAI 180
Db 120 AGARIHTNSGAPVNGAYTANSRQVDEYVRNNDMTLVFAAGNEGPNSTISAPGTAKNAI 179

QY 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAPGTIFILSARSSLPDSSF 240
Db 180 TVGATENRPSFGSLADPNHIAQFSRGATRDGRIKPDVAPGTIFILSARSSLPDSSF 239

QY 241 WANHDSKYAVMGGTSMATPIVAGNVAQLREHFVKNGRTTPKPSLLKAALIAAGADIGLY 300
Db 240 WANYSKYAVMGGTSMATPIVAGNVAQLREHFVKNGRTTPKPSLLKAALIAAGADIGLY 299

QY 301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPKIKISLVMSDAPASTTA 360
Db 300 PSGDQGWGRVTLDKSLNAVYVNEATATAGQKATYSFQQAQKPKIKISLVMTDAPGSTTA 359

QY 361 SVTLVNDLDLVITAPNGTYVGNDFTPYDNDWGRNNVENFINAPQSGTYTIEVQAYN 420

Query Match 88.8%; Score 1994.5; DB 2; Length 433;
Best Local Similarity 87.6%; Pred. No. 9.5e-123;
Matches 380; Conservative 26; Mismatches 25; Indels 1; Gaps 1;

QY 1 NDVARGIVKADVAAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
Db 1 NDVARGIVKADVAAQNYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60

QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 61 NANDPNGHGHVAGSVLGN-ALNKGMAPOANLVFQSIMDSGGGLGGLPSNLTLFQAWN 119

QY 121 AGARIHTNSGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGTISAPGTAKNAI 180
Db 120 AGARIHTNSGAPVNGAYTANSRQVDEYVRNNDMTLVFAAGNEGPNSTISAPGTAKNAI 179

QY 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAPGTIFILSARSSLPDSSF 240
Db 180 TVGATENRPSFGSLADPNHIAQFSRGATRDGRIKPDVAPGTIFILSARSSLPDSSF 239

QY 241 WANHDSKYAVMGGTSMATPIVAGNVAQLREHFVKNGRTTPKPSLLKAALIAAGADIGLY 300
Db 240 WANYSKYAVMGGTSMATPIVAGNVAQLREHFVKNGRTTPKPSLLKAALIAAGADIGLY 299

QY 301 PNGNQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPKIKISLVMSDAPASTTA 360
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Db 300 PSQGQGRVTLDKSLNVAAYNEATALTGQKATYSFQTAGKPLKLSLWTDAPGSTTA 359
Qy 361 SVTLVNDLVLITAPNGTOYVGNDFSTPYNDNDWGRNNVNFVFNAPQSGTYTIEVOAYN 420
Db 360 SYTLVNDLVLITAPNGQKYVGNDFSPYDNDNDWGRNNVNFVFNAPQSGTYTIEVOAYN 419
Qy 421 VPVGPQTFSLAIVN 434
Db 420 VPSGQRFSLAIVH 433

RESULT 7
Q9AQR2_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROC;
OS Bacillus sp. Y.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133779;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RX MEDLINE=20568675; PubMed=1118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046404; BAB21267.1; -; Genomic_DNA.
DR HSP; Q45670; 1BFI.
DR SMR; Q9AQR2; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_S8_S53.
DR InterPro; IPR000209; Peptidase_S8; 1.
DR Pfam; PF00482; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON TER 1
FT TER 433
SQ SEQUENCE 433 AA; 45588 MW; B81291A803C775AE CRC64;

Query Match 88.5%; Score 1987.5; DB 2; Length 433;
Best Local Similarity 87.3%; Pred. No. 2.7e-122;
Matches 379; Conservative 29; Mismatches 25; Indels 1; Gaps 1;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQNNVGLYQGGQVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDGGGGLGGLPSNLQTLFSQAYS 120
Db 61 NASDPNGHGHVAGSVLNGN-ALNKGMAPQANLVFQSIMDSSGGLGGLPSNLTLFSQAWN 119

Qy 121 AGARIHNSWGAAYNGAYTTDSRVVDYVRKNDMTILFAAGNEPNGGTTISAPCTAKNAI 180
Db 120 AGARIHNSWGAAYNGAYTANSRQVDEYVRNDMTILFAAGNEPNSGTTISAPCTAKNAI 179

Qy 181 TVGATENLRPSFGSYADININHAQVSSRGPTKGRIPKDVMAPTFTILSRSSLPDSSF 240
Db 180 TVGATENVRPSFGSIANDPNHIAQVSSRGATRGRIKPDVTAPTFTILSRSSLPDSSF 239

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGADIGLY 300
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Db 240 WANYSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGADIGLY 299
Qy 301 PNCNQGWRVTLDKSLNVAAYNEATALTGQKATYSFQTAGKPLKLSLWSDAPASTTA 360
Db 300 PNCNQGWRVTLNKSUNVAAYNEATALTGQKATYSFQAGKPLKLSLWTDAPGSTTA 359
Qy 361 SVTLVNDLVLITAPNGTOYVGNDFSTPYNDNDWGRNNVNFVFNAPQSGTYTIEVOAYN 420
Db 360 SYTLVNDLVLITAPNGQKYVGNDFSPYDNDNDWGRNNVNFVFNAPQSGTYTIEVOAYN 419
Qy 421 VPVGPQTFSLAIVN 434
Db 420 VPSGQRFSLAIVH 433

RESULT 8
Q4NB18_9MICC PRELIMINARY; PRT; 697 AA.
AC Q4NB18;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin.
GN ORFNames=ArthDRAFT_0589;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococciaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (PGF-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHG01000025; EAL94539.1; -; Genomic_DNA.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 697 AA; 73821 MW; B8924966C67C0714 CRC64;

Query Match 38.7%; Score 870.5; DB 2; Length 697;
Best Local Similarity 41.4%; Pred. No. 1.1e-48;
Matches 209; Conservative 73; Mismatches 138; Indels 85; Gaps 14;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGR-T- 59
Db 196 NNVAEILNADVQLNGTTRVAGGEVAVADTGTDTG-DAANPHPAFTGRVQTLVALGR-TA 254

Qy 60 -NNANDTNGHGHVAGSVLNGSTN-----KGMAPQANLVFQSIMDSSGGLGGLPSNLQ 112
Db 255 PDKADDPHGHTVAGSVLGRGNSATWGGAIEGTAPEALLILOSLDLPNGGLGGIPVNLN 314

Qy 113 TLFQAYSAGARHTNSWGA-AVNGAYTTDSRVVDYVRKN-DMTILFAAGNEPNG- 167
Db 315 DLFQKTYDGGARVHTNSWGVPLNLPYDASSRDEIDFVNHDPQVCFAGNAGNDGVGNSD 374

Qy 168 -----GTISAPGTAKNAITVGATENLR-----PSFGSY-----ADNINHA 203
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Db 375 GTVDSNIGSSAAKNCITVGSLSLRKEFTPTSGTYWPGDFPAPNPKVRDQKQANPPGMV 434
Qy 204 QFSRGPTKQRIKPDVMPAGTFTILSRSSLP-DSSFANHDSKYAYMGTSMTATPIVA 262
Db 435 AFSSRGPTKEGRIKPDVVPAGTSTILSLRNAPMGNTFGTSTDPFLFFDSTGTSMTATPIVA 494
Qy 263 GNVAQLREHFVNKRGITPKPSLLKALIAAGADIGLGY-----PNGNCGWGRVTLDK 314
Db 495 GCAAALRETLVKNGLNPSAALVALLVNGADVLPQQYNPSEAGESPNSGNGWGRVNLAR 554
Qy 315 SLNW-----AYVNESSLSLSQKATYSF-----TATAGKP 344
Db 555 SVLPGQPNAGLGGGPLEGQSDFTIDPEVPKVAAGRRNRGPAAPALTAAGVT 614
Qy 345 LKISLVMSDAPASTTASVTLVNDLVLITAPNGTYGVNDFTSPYNDWNGRNVNFI 404
Db 615 LKITLVMSDPPGP-----QLQNDLVLVLAADGSRHGNSTGA---GFDRRNVEQVLW 666
Qy 405 NAPSQGTVTIEVQYVNVPGQTS 429
Db 667 TGMPPGQAVIVRAFRITQFPQPYA 691

RESULT 9
Q6MKR4 DBEBA
ID Q6MKR4 DBEBA PRELIMINARY; PRT; 711 AA.
AC Q6MKR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Subtilisin-like serine protease precursor.
GN OrderedLocustNames=Bd2321;
OS Bdelovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842652; CAE80143.1; -; Genomic_DNA.
DR HSP; P27693; 1AH2.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Complete proteome; Protease; Signal.
FT SIGNAL 1 8 Potential.
SQ SEQUENCE 711 AA; 74914 MW; 4930050843357E5 CRC64;

Query Match 33.6%; Score 754.5; DB 2; Length 711;
Best Local Similarity 37.9%; Pred. No. 4.8e-41;
Matches 180; Conservative 77; Mismatches 145; Indels 73; Gaps 13;

Qy 18 GLYGQGVAVADTGLDTRNDSSMHEAFPRGKITALYALGRTNNA-NPTNGHGHVAGSV 76
Db 243 GYAGKGVQVSMADTGLDSG-NTGAHQDPAGGVISGYPFGLWSKWSMDPMGHGTHVAGSV 301
Qy 77 LQNGSTNKG-----APQANLVFQSTMDSCGGLGLPSNLQTLFSAQYAGARIHTNSWGA 132
Db 302 MGRGTASKGLLKGGAYEAMVAGMWSMMKNLSVPSGLDLFEKAFADGARIHTNSWG 361
Qy 133 A-VNGAYTTDSNRVDYVRKN-DMTILFAAGNEP-----NGGTISAPGTAKNAITV 182
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Db 362 ARTFGAYDPAVQVDEWSYANPDMILFPAAGSGADKNKDKGRIDSNMASPGTAKNVLTV 421
Qy 183 GATENL-----RPSFGSY-ADNINHAQVSSSRGPTKGRIKPD 219
Db 422 GASENVTKSGGIQVPIISKLRAAKDEWPESEPIYSSYISDNGNGLAMFSSRGPTTDTGRTPD 481
Qy 220 VMAPGTFTLSARSGLAPDSSFWANHDSKYAYMGTSMTATPIVAGNVAQLREHFVNKRGIT- 278
Db 482 IVAPGTNVLSVFOEKDASPLMGAYNKDYVMSGTSMATPLAAGAAIAIAKQVLVEKLGMMK 541
Qy 279 TPXPSLILKAALIAAGADIGLGY-----PNGNCGWGRVTLDKSLNVA--- 319
Db 542 NPSAALMKATMLHTAVDMYGFQGEIGAARGQELLTERPNSDGYGRVDVANIANLGAT 601
Qy 320 -YNESSLSLSQKATYSFTATAGKPLKISLVMSDAPASTTASVTLVNDLVLITAPNGT 378
Db 602 QFVDNRQVGAAGAEVSEFTLNAPGSLYANLVMTDAPGSANAAQALVNDLVLTPENGQ 661
Qy 379 QYVGNDFTPSYNDWNGRNVNFIAPQSGTYTIEVQYVNVPV---GPQTS 430
Db 662 TLSMNDHI-----NNLEMIKSLPAGTYKLTIVKGFQVPGKNGQAQAYAL 706

RESULT 10
Q4NVB5_9DELTA
ID Q4NVB5_9DELTA PRELIMINARY; PRT; 1748 AA.
AC Q4NVB5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin:Nepovirus coat
DE protein, N-terminal:Nepovirus coat protein, N-terminal precursor.
GN ORFNames=AdenHRAFT_3007;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHD0100011; EAL79523.1; -; Genomic_DNA.
KW Capsid protein; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 1748 AA; 177411 MW; BL56DE33BB81DE76 CRC64;

Query Match 32.9%; Score 739.5; DB 2; Length 1748;
Best Local Similarity 40.1%; Pred. No. 1.5e-39;
Matches 192; Conservative 66; Mismatches 154; Indels 67; Gaps 19;

Qy 1 NDVARGIVK-----ADVAQSSYGLVGQGVAVADTGLD-----TGRNDSMHEAFR 47
Db 248 NDTSRWITQTVGSDTSISDRGLGQGVAVIGTGLDHDACWFRDPIGAAGPMHR---- 304
Qy 48 KKITALYALGRTNANDTN-CHGTHVAGSVLGN-----GSTNKGMAPQANLVFQSIIDS 100
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Db 305 -KVAAYITVG--GDDYDGNLGHGTHVAGTQDPTITGAAANGMAPGVVVVTDLFLG 361
 Qy 101 GGGGLGGLPSNLQTLFQSAYSAGARIHTNSWGAAVNGAVYTTDSNRVDDYVRKN-DMTILFA 159
 Db 362 ENNWFSPPADLAETFTPYALGARIHTNSWGSSN-AYDALARSADRFMEHPDFVLFA 420
 Qy 160 AGNEGPNGGTISAGTAKNAITVGATENLRPSFGSYADNINHVAQFSRSGPTKDKRIKPD 219
 Db 421 NGNAGPDVGSVGPATARNVSVGATGN-----GLAAED---VASFSSHGPAADGRKTPT 472
 Qy 220 VMAPGTILSARSLAPDSSFWANHDSKYAVMGCTSMATPIVAGNVQAQLREHFVN---R 276
 Db 473 LTAPEGVIVSADSGTPTAS-----NCSVTAP-SGTSMATPAAAGAAALVRQYFEGGFWPS 527
 Qy 277 GI-----TPKSLKKAALIAGAADI-----GLG-YPNGNGMGWGRVTLDKSLNVA----- 319
 Db 528 GLGSPADARSFSAALVKATLVNSAQVAGENGNGPISTGGWGRINLSNALRFAADAAY 587
 Qy 320 --YVNESSLSSTOKATYSFTATAGKPLKISLWSDAPASTTASVTLVNDLIDLVTAPNG 377
 Db 588 LDVVEVAAGLETGSGTQRFVSTGAQPLKLTWTDAPGSQLADRSILVNDLIDLAVTVPGG 647
 Qy 378 -TQVVGNDFT---SPYNDNDGRNVNFINAPQSGTYTIEVOAYNVVPGQPTFSLAI 432
 Db 648 ATTILGNVVALGESVAGGAPDLNLVBEQVLLAAPTGTVTYTVRTGYNVVPGQPFALVI 706

RESULT 11
 Q4HUY5_GIBZE
 ID Q4HUY5_GIBZE PRELIMINARY; PRT; 1088 AA.
 AC Q4HUY5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=FG11223.1;
 OS Gibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=229533;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PH-1;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArelano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schuppback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR ENBL; AACW01000460; EAA75433.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 1088 AA; 119629 MW; E3B38CB94C07F542 CRC64;

Query Match 26.3%; Score 592; DB 2; Length 1088;
 Best Local Similarity 35.6%; Pred. No. 4e-30;
 Matches 181; Conservative 71; Mismatches 170; Indels 86; Gaps 24;

Qy 1 NDVAGIVKADVAQSSYGLYGQGIIVADPTGLDGTGRNDSSM-----HEAPRGKITALYAL 56
 Db 581 NDLAETELNANILALSTSYEGNGQKVCVADTGTDOGMADMGILVHPAFNGRVEHLEAL 640
 Qy 57 GRTNNANDTNGHGTAVAGSVLNGSTN-----KGMAPQANLVFQST-----MDSGGGLGG 106
 Db 641 W-LGDSKDTAGHGTVCASICGNGLYKNGDIRVGVAPGATLMVQSLAQVSRDPNKGAI 699
 Qy 107 LPSNL-QTLFQSAYSAGARIHTNSWGA---AVNG--AYTTDSNRVDDYV-RKNDMTILFA 159
 Db 700 VPMDLGLQLFNSPYKLYRHSNSGWKWDKATGQLGYEQAWDIDKFVIDHQDFVVLVA 759
 Qy 160 AGNEGPNGGT-----ISAPGTAKNAITVGATENLRPSFGSYADN-----INHVAQFS 206
 Db 760 AGNNAEKAKSKSNHIGAAGSAFCITVGATGTTTPNNNDYGFNEVGAKPMTRINDTAKFS 819
 Qy 207 SRGPTKD-----GRIKPDVMAPTGFIILSARS-SLAPDS-----SPWANHDSKYAYM 251
 Db 820 SRGPTKPGRDINGNEVAGRIKPDVAPGVALLSAAARAKOSRNRVMYGRGTGDDMTFM 879
 Qy 252 GGTSMATPIVAGNVQAQLREHFVNRGITPKPSLLKKAALIAGAAD-----IGLGYPNGNQ 305
 Db 880 SGTSMTPLVAGCVALLREALKHEKKEKPSAALI KALLVNGAVNFSQGLGLGY-DYDQ 938
 Qy 306 GWCGRVTLDKSLNV-----AYVNESSLSSTSQ-----KATYS-FTATAGK-PL 345
 Db 939 GFCRVDDIDSSISMVKLSFSFVGGKLFEDTQFDVAPLRQVPEERRRWTSSLPVPAGNRNL 998
 Qy 346 KISLWSDAPASTTASVTLVNDLIDLVTAPNGTYVGNDFTSYVNDWDCGRNVNFIN 405
 Db 999 TVTLAYLPDPAQ---SGLMNDNLNLIVLS-GGAERHGNMGKGP---GYDHTNNVEKLIWE 1051

Qy 406 APOSGTYTIEVQAY-NVVP-GPQTFSILA 431
 Db 1052 NVPGTTFKIVASIMWIDVKAPTSFAVA 1079

RESULT 12
 Q747P6 GEOSL
 ID Q747P6 GEOSL PRELIMINARY; PRT; 2030 AA.
 AC Q747P6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Fibronectin type III domain protein.
 GN OrderedLocusNames=GSU3219;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Maduprat R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gunn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
 RA Van Aken S.B., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 RT environments";
 RL Science 302:1967-1969(2003).
 DR ENBL; AS017180; AAR36610.1; -; Genomic_DNA.
 DR HSSP; P27693; 1AH2.
 DR TIGR; GSU3219; -.
 DR GO; GO:0004289; F:subtilase activity; IEA.


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Db 725 MSNHLVNNNNNNNNKTSIGITKFGVIGGLDLRLVKPNQWKEESLSLTCQNTSYCTYK 784
Qy 339 -----ATAGKPLK---ISLVMSDAPASTTASVTLVNDLDLVI-----TAPNGT 378
Db 785 PSSSSSSGNNIPRVAVTLVWTDPPSVAGAKFNLVNNLDLTMIIYRONGSTIFYSNQGS 844
Qy 379 QYVGNDFTSYNDWMDGRNNVNFVINAPOSQTYTIEVOAYNVVPGQTF 429
Db 845 SFLG---LAPTQDT---LNNVEGIVHNPTERTMYRENVAGTNVPMGPQNS 889

RESULT 14
TAGC DICDI
ID TAGC DICDI STANDARD; PRT; 1743 AA.
AC Q23868;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prestalk-specific protein tagC precursor (BC 3.4.21.-).
GN Name:tagC;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=AX4;
RX MEDLINE=97140317; PubMed=8986798; DOI=10.1073/pnas.93.26.15260;
RA Shauleky G., Escalante R., Loomis W.F.;
RT "Developmental signal transduction pathways uncovered by genetic suppressors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
CC -!- FUNCTION: Intercellular communication via tagC may mediate integration of cellular differentiation with morphogenesis (By similarity).
CC -!- SIMILARITY: Contains 1 ABC transmembrane type-1 domain.
CC -!- SIMILARITY: Contains 1 ABC transporter domain.
CC -!- SIMILARITY: Contains 1 peptidase S8 domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC EMBL: U60086; AAB03331.1; -; mRNA.
CC PIR: T18279; T18279.
CC HSP; P08716; IMT0.
CC DictyBase; DDB0001795; tagC.
CC InterPro; IPR011527; ABC membrane 1.
CC InterPro; IPR011140; ABC_TM_transpt.
CC InterPro; IPR003439; ABC_transp_like.
CC InterPro; IPR002029; Pept_S8_S53.
CC Pfam; PF00664; ABC membrane; 1.
CC Pfam; PF00005; ABC_tran; 1.
CC Pfam; PF00082; Peptidase S8; 1.
CC PRINTS; PR00723; SUBTILISIN.
CC ProDom; PD000006; ABC transporter; 1.
CC PROSITE; PS50928; ABC_TM1F; 1.
CC PROSITE; PS50929; ABC_TRANSPORTER_1; 1.
CC PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
CC PROSITE; PS00136; SUBTILASE ASP; FALSE_NEG.
CC PROSITE; PS00137; SUBTILASE HIS; 1.
CC PROSITE; PS00138; SUBTILASE_SER; FALSE_NEG.
KW ATP-binding; Glycoprotein; Hydrolase; Nucleotide-binding; Protease;
KW Serine protease; Signal; transmembrane; transport.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 1743 Prestalk-specific protein tagC.
FT TRANSMEM 962 982 Potential.
FT TRANSMEM 1027 1047 Potential.
FT TRANSMEM 1072 1092 Potential.
FT TRANSMEM 1157 1177 Potential.
FT TRANSMEM 1260 1280 Potential.
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FT TRANSMEM 1288 1308 Potential.
FT DOMAIN 1031 1314 ABC transmembrane type-1.
FT DOMAIN 1450 1687 ABC transporter.
FT NP_BIND 1485 1492 ATP (Potential).
FT REGION 316 642 Serine protease.
FT COMPBIAS 42 46 Poly-Asn.
FT COMPBIAS 94 103 Poly-Asn.
FT COMPBIAS 643 646 Poly-Ala.
FT COMPBIAS 733 741 Poly-Asn.
FT COMPBIAS 786 792 Poly-Ser.
FT COMPBIAS 1337 1340 Poly-Glu.
FT COMPBIAS 1346 1352 Poly-Gly.
FT COMPBIAS 1353 1357 Poly-Asn.
FT COMPBIAS 1358 1364 Poly-Asp.
FT COMPBIAS 1381 1386 Poly-Asn.
FT COMPBIAS 1707 1729 Poly-Asn.
FT ACT_SITE 325 325 Charge relay system (By similarity).
FT ACT_SITE 372 372 Charge relay system (By similarity).
FT CARBOHYD 390 390 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 547 547 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 614 614 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 689 689 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 735 735 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 741 741 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 776 776 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 832 832 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 887 887 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1251 1251 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1385 1385 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1386 1386 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1454 1454 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1704 1704 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1743 AA; 194146 MW; 12DB363E2F729839 CRC64;

Query Match 23.3%; Score 523.5; DB 1; Length 1743;
Best Local Similarity 27.9%; Pred. No. 2.3e-25;
Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;

Qy 19 LYQGOIVAVATGTLTGR---NDS-----SMHEAFRGKITALYALGFTNNANDTNGH 68
Db 314 LRKGGQILSIADTGLDGHCHFFSDSKYPIPLNSVLNHR-KVVTYITTSDDSDKVDGH 372
Qy 69 GTHVAGSVLG-----NGSTNKGMAPQANLVFQSIMDSGGGLGGL--PSNLTLFSQAY 119
Db 373 GTHICGSAAGTPEDSSVNISSFGLATDAKIAF--FDLASGSSSLTFPSDLKQLQPLY 429
Qy 120 SAGARIHTNSWGA---AVNGAYTTDSRNVDYVRKN-DWTILFAAGNPGNGGTIS--A 172
Db 430 DAGARVHCDSWGVSVEGVTGYSSTASIDDFLTHPDPFIILRAAGN---NEQYLSLLT 486
Qy 173 PGTAKNAITVGATENLR-----PSGSYADNI----- 199
Db 487 QSTAKNVIITGAHQTHENYLTDPNINYNQSSVDINQELICDFDSRYCNYTTAQCCLES 546
Qy 200 -----NHVAQFSSRGPTKDGRIKDPVMAPGTFIL 228
Db 547 NATTGLASCCPTLLRKSVIDAANTQPLLNNENNICSFSSKGPETHDGMKALVAPGEYIT 606
Qy 229 SARSSIA-----PDSSFANHDSKYVMGTSMTATPIVAGNVAQLREH-----F 272
Db 607 SARNSGANTTDQCGDGLS-PNTNALLA-ISGTSMATSFAAAAATILRQYLVVDGYPTGSI 664
Qy 273 VKNRGITTPKPSLLKALIAQA-----ADIGLYPNGN-----QGWGRVT 311
Db 665 VESNKLOPTGSLKALMINNAQLLNGTFQLTITSSSITYPSNQVFENFAGASLVQGGAIR 724
Qy 312 LDKSLNAVYVNESS-----SLTSQKATYSFT-- 338
Db 725 MSNHLVNNNNNNNNKTSIGITKFGVIGGLDLRLVKPNQWKEESLSLTCQNTSYCTYK 784
Qy 339 -----ATAGKPLK---ISLVMSDAPASTTASVTLVNDLDLVI-----TAPNGT 378
```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 30, 2006, 08:25:46 ; Search time 189 Seconds
(without alignments)
1008.944 Million cell updates/sec

Title: US-10-820-712A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAVNPVGPQTFLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

A_Geneseq_21:*
1: Genesexp1990s:*
2: Genesexp1990s:*
3: Genesexp2000s:*
4: Genesexp2001s:*
5: Genesexp2002s:*
6: Genesexp2003as:*
7: Genesexp2003bs:*
8: Genesexp2004s:*
9: Genesexp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2247	100.0	434	5	AAM50080
2	2247	100.0	434	7	ADY33778
3	2247	100.0	434	7	ADZ51757
4	2247	100.0	434	8	ADL25802
5	2247	100.0	434	8	ADM40771
6	2247	100.0	434	8	ADSL4427
7	2247	100.0	434	8	ADT49604
8	2247	100.0	640	2	AAV17090
9	2247	100.0	640	8	ADM40773
10	2247	100.0	640	8	ADSL4437
11	2247	100.0	641	8	ADT49613
12	2242	99.8	434	8	ADM40780
13	2242	99.8	434	8	ADSL4441
14	2242	99.8	640	2	AAV17091
15	2239	99.6	434	8	ADSL4438
16	2239	99.6	434	8	ADSL4442
17	2238	99.6	434	8	ADSL4439
18	2232	99.3	434	8	ADSL4440
19	2230	99.2	434	8	ADSL4443
20	2225	99.0	434	8	ADSL4444
21	2210	98.4	434	8	ADSL4445
22	2195	97.7	436	8	ADM40787
23	2191	97.5	434	5	AAM50081
24	2191	97.5	434	7	ADZ51758

```

98 2112.5 94.0 433 8 ADS52081 AdS52081 Bacillus
99 2112.5 94.0 433 8 ADS52029 AdS52029 Bacillus
100 2112.5 94.0 433 8 ADS52015 AdS52015 Bacillus

ALIGNMENTS

RESULT 1
ID AAM50080 standard; protein; 434 AA.
AC AAM50080;
XX
XX
DT 12-AUG-2002 (first entry)
DE
DE Bacillus sp KSM-KP43 alkaline protease protein fragment.
KW Alkaline protease; detergent; laundry; bleaching; dishwasher.
XX
OS Bacillus sp.
XX
XX EPI209233-A2.
XX 29-MAY-2002.
XX
XX 22-NOV-2001; 2001EP-00127851.
XX
XX Hatada Y, Ogawa A, Kageyama Y, Sato T, Araki H, Sumitomo N;
PI Okuda M, Saeki K;
XX
XX WPI; 2002-437518/47.
XX
XX New modified alkaline proteases useful in detergent compositions.
XX
XX Claim 1; Page 10-11; 25pp; English.
XX
XX This invention describes novel Bacillus sp. alkaline proteases useful in
CC detergent compositions, especially in laundry, bleaching or automatic
CC dishwasher detergents. The novel proteases have an increased detergency &
CC (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This
CC sequence represents a fragment of the alkaline protease KP43 from
CC Bacillus sp strain KSM-KP43 which is used to create the modified protease
CC represented in AAM50090
XX
XX SQ Sequence 434 AA;
XX
XX Query Match 100.0%; Score 2247; DB 5; Length 434;
XX Best Local Similarity 100.0%; Pred. No. 6.4e-159;
XX Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
Qy 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Qy 121 AGARIHTNSGAAVNGAYTTDSRNVDVYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSGAAVNGAYTTDSRNVDVYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSVADNINHAQFSSRGPTKQGRKPDVMAQPTFILSARSSLAPSSSF 240
Db 181 TVGATENLRPSFGSVADNINHAQFSSRGPTKQGRKPDVMAQPTFILSARSSLAPSSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFVNKRGITPKPSSLKKAALIAGADIGLY 300

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Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFVNKRGITPKPSSLKKAALIAGADIGLY 300
Qy 301 PNGNQGWGRVTLDKSLNVAIVNNESSLSSTSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNVAIVNNESSLSSTSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLDLVIITAPNGTQYVGNDFTSYNDNDGNNVENVFINAPQSGTYTIEVOAYN 420
Db 361 SVTLVNDLDLVIITAPNGTQYVGNDFTSYNDNDGNNVENVFINAPQSGTYTIEVOAYN 420
Qy 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 2
ADY33778
ID ADY33778 standard; protein; 434 AA.
XX
AC ADY33778;
XX
XX 05-MAY-2005 (first entry)
XX
DE Bacillus species alkaline protease.
XX
KW mutagenesis; alkaline protease; detergent; laundry; cosmetic; food;
KW bleaching detergent.
XX
OS Bacillus sp.
XX
XX EPI347044-A2.
XX
XX 24-SEP-2003.
XX
XX 21-MAR-2003; 2003EP-00006472.
XX
XX 22-MAR-2002; 2002JP-00081428.
XX 06-JUN-2002; 2002JP-00165987.
XX 18-OCT-2002; 2002JP-00304230.
XX 18-OCT-2002; 2002JP-00304231.
XX
XX (KAOS ) KAO CORP.
XX
XX Okuda M, Sato T, Saito K, Sumitomo N, Izawa Y, Saeki K;
XX Kobayashi T, Nomura M;
XX
XX WPI; 2003-846540/79.
XX N-PSDB; ADY33779.
XX
XX New alkaline protease having specific amino acid residue at a specific
XX position of its amino acid sequence, useful for producing detergent
XX compositions, laundry detergent, fiber modifiers, leather-treating agents
XX or pipe cleaners.
XX
XX Claim 1; SEQ ID NO 1; 31pp; English.
XX
XX The invention relates to an alkaline protease having a fully defined
XX sequence of 434 amino acids (I) given in the specification, or an amino
XX acid sequence at least 80% homology with (I), where an amino acid residue
XX at position 65, 101, 163, 170, 171, 273, 320, 359 or 387 of (I) is
XX selected from 16 amino acid residues. The amino acid residues at the
XX corresponding positions are selected from: position 65: proline; position
XX 101: asparagines; position 163: histidine, aspartic acid, phenylalanine,
XX valine, asparagine, serine, isoleucine, leucine, glutamine, threonine or
XX valine; position 170: valine or leucine; position 171: alanine, glutamic
XX acid, glycine or threonine; position 273: isoleucine, glycine or
XX threonine; position 320: phenylalanine, valine, threonine, leucine,
XX isoleucine or glycine; position 359: serine, leucine, valine, isoleucine
XX or glutamic acid; and position 387: alanine, lysine, glutamine, glutamic
XX acid, arginine or histidine. The alkaline protease is useful for the
XX production of a detergent composition, such as laundry detergent, fiber
XX modifiers, leather-treating agents, cosmetic compositions, bath

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CC additives, food modifiers and pharmaceutical compositions. The alkaline
CC protease may also be used as bleaching detergent, hard surface cleansing
CC detergent, pipe cleaner, artificial tooth cleaner, and as a sterilizing
CC cleaner for medical tools. The new alkaline protease has a more potent
CC proteolytic capacity, exhibiting excellent detergency for the removal of
CC a complex stain, and has high secretion capacity. This sequence
XX corresponds to the Bacillus sp. alkaline protease.
SQ Sequence 434 AA;

Query Match 100.0%; Score 2247; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPTFILSARSSSLAPDSSF 240
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPTFILSARSSSLAPDSSF 240
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 300
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 300
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVENFINAPQSGTYTIEVQAYN 420
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVENFINAPQSGTYTIEVQAYN 420
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 VPVGPOTFSLAIVN 434
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 VPVGPOTFSLAIVN 434
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
ADZ51757
ID ADZ51757 standard; protein; 434 AA.
XX AC ADZ51757;
XX DT 16-JUN-2005 (first entry)
XX DE Wild-type Bacillus sp. alkali protease.
XX KW alkali protease; enzyme; surfactant; mutagenesis.
XX OS Bacillus sp.
XX PN JP2003125783-A.
XX PD 07-MAY-2003.
XX PF 26-OCT-2001; 2001JP-00329472.
XX PR 26-OCT-2001; 2001JP-00329472.
XX PA (KAOS) KAO CORP.
XX DR WPI; 2003-856569/80.
XX

PT New alkali protease useful for preparing detergents comprises
PT substitution mutations at 251 or 256 position of protease KP43 derived
XX from Bacillus species KSM-KP43.
XX Claim 1; SEQ ID NO 1; 16pp; Japanese.
XX The invention relates to a mutant alkali protease having an amino acid
CC deletion at position(s) 251 or 256 in a fully defined sequence given as
CC SEQ ID No:1 in the specification, or the following amino acid residue
CC Asp, Gly, Ala, Asp, Thr, Ile, Val, Leu or Glu at position 251, or the
CC amino acid residue Lys, Ser, Phe, Arg, Tyr, Met, Thr, Ile, Val, Leu, or
CC Glu at position 256. Also described are: (i) an alkali protease having to
CC the amino acid sequence of SEQ ID No:1, or having 60% or more homology to
CC SEQ ID No:1, or a deletion of amino acid corresponding to position 251 or
CC 256, (ii) a gene which encodes an alkali protease, (iii) a recombinant
CC vector containing the gene, and (iv) a transformed organism containing
CC the recombinant vector. The alkali protease sequence having 60% or more
CC homology to SEQ ID No:1 is chosen from a fully defined sequence selected
CC from SEQ ID Nos 2-7 as given in the specification. The transformed
CC organism is a microorganism. The mutant alkali protease is useful for
CC preparing detergents. The mutant alkali protease exhibits high resistance
CC against oxidizing agent. The mutant alkali protease has high specific
CC activity. This sequence represents wild-type Bacillus sp. alkali
XX protease.
SQ Sequence 434 AA;

Query Match 100.0%; Score 2247; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPTFILSARSSSLAPDSSF 240
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPTFILSARSSSLAPDSSF 240
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 300
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 300
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVENFINAPQSGTYTIEVQAYN 420
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVENFINAPQSGTYTIEVQAYN 420
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 VPVGPOTFSLAIVN 434
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 VPVGPOTFSLAIVN 434
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
ADL25802
ID ADL25802 standard; protein; 434 AA.
XX AC ADL25802;
XX DT 20-MAY-2004 (first entry)
XX DE Bacillus alkaline protease.

XX alkaline protease; washing agent; enzyme.
 KW Bacillus sp.
 OS JP2004008085-A.
 XX PD 15-JAN-2004.
 XX PF 06-JUN-2002; 2002JP-00165950.
 XX PR 06-JUN-2002; 2002JP-00165950.
 XX PA (KAOS) KAO CORP.
 XX WI; 2004-094297/10.
 XX DR N-PSDB; ADL25803.
 XX PT Novel mutant alkaline protease produced by substituting the amino acid
 PT residues useful as washing agent.
 XX Claim 1; SEQ ID NO 1; 21pp; Japanese.
 XX The invention comprises a mutant Bacillus alkaline protease which
 CC contains substitutions at positions 163, 170 and 434. The mutant alkaline
 CC protease is useful as a washing agent. The present amino acid sequence
 CC represents a Bacillus alkaline protease of the invention.
 XX Sequence 434 AA;
 SQ
 Query Match 100.0%; Score 2247; DB 8; Length 434;
 Best Local Similarity 100.0%; Pred. No. 6.4e-159;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
 DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
 QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIQSDSGGLGGLPSNLQTLFSQAYS 120
 DB 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIQSDSGGLGGLPSNLQTLFSQAYS 120
 QY 121 AGARIHTNSWGAANVGAVTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 121 AGARIHTNSWGAANVGAVTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 QY 181 TVGATENLRPFGSVADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSSSLAPDSSF 240
 DB 181 TVGATENLRPFGSVADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSSSLAPDSSF 240
 QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
 DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
 QY 301 PNGNQGWRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPLKISLVMSDAPASTTA 360
 DB 301 PNGNQGWRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPLKISLVMSDAPASTTA 360
 QY 361 SVTLVNDLDLVITAPNGTQYVGNDETSPYNDWNGRNNVNFVINAPOS GTTYIEVQAYN 420
 DB 361 SVTLVNDLDLVITAPNGTQYVGNDETSPYNDWNGRNNVNFVINAPOS GTTYIEVQAYN 420
 QY 421 VPVGQTFSLAIVN 434
 DB 421 VPVGQTFSLAIVN 434
 RESULT 5
 ADM40771
 ID ADM40771 standard; protein; 434 AA.
 XX
 AC ADM40771;
 XX

DT 01-JUL-2004 (first entry)
 XX Mature alkaline protease from Bacillus sp. KSM-KP43.
 XX alkaline protease; laundry detergent; bleaching agent; detergent;
 KW denture-cleaning agent; enzyme.
 XX Bacillus sp.; KSM-KP43.
 OS US2004072321-A1.
 PN 15-APR-2004.
 XX 09-JUN-2003; 2003US-00456479.
 XX 26-JUN-2002; 2002JP-00186387.
 XX 18-OCT-2002; 2002JP-00304232.
 XX (KAOS) KAO CORP.
 XX Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
 PI WI; 2004-328572/30.
 XX N-PSDB; ADM40772.
 DR New alkaline protease having a mutant prepro sequence where amino acid
 DR residues at positions 52, 75 and 142 are substituted with another amino
 PT acid residue, useful as enzyme component of laundry detergents, or
 PT bleaching agents.
 PT Claim 1; SEQ ID NO 2; 29pp; English.
 PS The invention relates to an alkaline protease having a prepro sequence.
 XX The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
 CC acid sequence having 80% homology or higher to SEQ ID NO: 1, or an amino
 CC acid residues at: (a) position 52 is substituted by aspartic acid or
 CC arginine; (b) position 75 is substituted by alanine or arginine; and (c)
 CC position 142 is substituted by lysine. The alkaline protease is useful as
 CC an enzyme which can be incorporated into laundry detergents, bleaching
 CC agents, detergents for cleaning hard surfaces or drainpipes, denture-
 CC cleaning agents, and detergents for sterilising medical apparatus. The
 CC present sequence represents mature alkaline protease from Bacillus sp.
 CC KSM-KP43.
 XX Sequence 434 AA;
 SQ
 Query Match 100.0%; Score 2247; DB 8; Length 434;
 Best Local Similarity 100.0%; Pred. No. 6.4e-159;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
 DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
 QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIQSDSGGLGGLPSNLQTLFSQAYS 120
 DB 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIQSDSGGLGGLPSNLQTLFSQAYS 120
 QY 121 AGARIHTNSWGAANVGAVTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 121 AGARIHTNSWGAANVGAVTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 QY 181 TVGATENLRPFGSVADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSSSLAPDSSF 240
 DB 181 TVGATENLRPFGSVADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSSSLAPDSSF 240
 QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
 DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
 QY 301 PNGNQGWRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPLKISLVMSDAPASTTA 360
 DB 301 PNGNQGWRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPLKISLVMSDAPASTTA 360

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QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNMDGRNNVENVFNAPOSGTYTIEVOAYN 420
|||
DB 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNMDGRNNVENVFNAPOSGTYTIEVOAYN 420
|||
QY 421 VPVGPQTFSLAIVN 434
|||
DB 421 VPVGPQTFSLAIVN 434
|||

RESULT 6
ADSI4427
ID ADSI4427 standard; protein; 434 AA.
XX
AC ADSI4427;
XX
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease KP43 mature protein SEQ ID NO:1.
XX
KW protease; enzyme; alkaline protease; laundry detergent; KP43.
XX
OS Bacillus sp.; KSM-KP43.
XX
PN EPI466962-Al.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008604.
XX
PR 10-APR-2003; 2003JP-00106709.
XX
PA (KAOS ) KAO CORP.
XX
PI Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
XX
WPI; 2004-711313/70.
XX
DR N-PSDB; ADSI4428.
XX
New engineered alkaline protease, useful particularly in laundry
PT detergents, comprising specified amino acids at particular positions.
XX
Claim 1; SEQ ID NO 1; 31pp; English.
XX
PS
XX
The invention relates to a novel alkaline protease. The new alkaline
CC protease comprises an amino acid sequence in which one or more amino acid
CC residues selected from those located at 7 specific positions within
CC ADSI4427, or at positions corresponding to these positions are: position
CC 15 (histidine), position 16 (threonine or glutamine), position 166
CC (glycine), position 167 (valine), position 187 (serine), position 346
CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents the wild-type Bacillus sp. KSM-KP43 alkaline
CC protease, KP43.
XX
SQ Sequence 434 AA;

Query Match 100.0%; Score 2247; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAOSSYGLYGGQIVAVADTGLDTRNDSSMHFAFRGKITALVALGRTN 60
DB 1 NDVARGIVKADVAOSSYGLYGGQIVAVADTGLDTRNDSSMHFAFRGKITALVALGRTN 60
|||

QY 61 NANDTNGHGHVAGSVLNGSTNGKMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNGKMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
|||

QY 121 AGARIHNSGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
|||
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QY 1 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLTGRNDSSMHEAPRGKITALYALGRTN 60
 DB 1 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLTGRNDSSMHEAPRGKITALYALGRTN 60
 QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
 DB 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
 QY 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 QY 181 TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAFGTILSARSSLPDSSF 240
 DB 181 TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAFGTILSARSSLPDSSF 240
 QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAAGADIGLY 300
 DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAAGADIGLY 300
 QY 301 PNGQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPKISLVMSDAPASTTA 360
 DB 301 PNGQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPKISLVMSDAPASTTA 360
 QY 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDGRNNVENVFNAPOSQGTYYTIEVQAYN 420
 DB 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDGRNNVENVFNAPOSQGTYYTIEVQAYN 420
 QY 421 VPVGPQTFSLAIVN 434
 DB 421 VPVGPQTFSLAIVN 434

RESULT 8
 AAY17090
 ID AAY17090 standard; protein; 640 AA.
 AC AAY17090;
 XX
 DT 20-MAR-2003 (revised)
 DT 21-JUL-1999 (first entry)
 DE Bacillus alkaline protease.
 XX
 KW Alkaline protease; Bacillus; casein digestion; oleic acid; enzyme;
 KW washing composition; oxidising agent.
 XX
 OS Bacillus sp.
 XX
 PN WO9918218-A1.
 XX
 PD 15-APR-1999.
 XX
 PF 07-OCT-1998; 98WO-JP004528.
 XX
 PR 07-OCT-1997; 97JP-00274570.
 XX
 XX (KAOS) KAO CORP.
 XX
 PI Takaiwa M, Okuda M, Saeki K, Kubota H, Hitomi J, Kageyama Y;
 PI Shikata S, Nomura M;
 XX
 DR WPI; 1999-287736/27.
 DR N-PSDB; AAX3278.
 XX
 XX Alkali protease from Bacillus used in washing powders.
 PT
 PS Disclosure; Page 58-63; 71pp; Japanese.
 XX
 CC The invention relates to alkaline proteases produced by strains of
 CC Bacillus. The proteases ability to digest casein is not inhibited by
 CC oleic acid and they have a high stability to oxidising agents. The
 CC alkaline protease of the invention has the following properties: (a) it

CC is active over the pH range 4-13 and has at least 80% of its optimum
 CC activity over the range pH 6-12; (b) after 30 minutes at 40 deg. C it is
 CC stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d)
 CC its ability to digest casein is not inhibited by oleic acid; (e) it has
 CC molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be
 CC used as enzymes in washing compositions for use in automatic dishwashers
 CC and for washing clothes. The stability to oxidising agents allows the
 CC enzyme to be an effective component of washing compositions including
 CC bleaches. The present sequence represents an alkaline protease. (Updated
 CC on 20-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 640 AA;

Query Match 100.0%; Score 2247; DB 2; Length 640;
 Best Local Similarity 100.0%; Pred. NO. 1.le-158;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLTGRNDSSMHEAPRGKITALYALGRTN 60
 DB 207 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLTGRNDSSMHEAPRGKITALYALGRTN 266
 QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
 DB 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 326
 QY 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 327 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
 QY 181 TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAFGTILSARSSLPDSSF 240
 DB 387 TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAFGTILSARSSLPDSSF 446
 QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAAGADIGLY 300
 DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAAGADIGLY 506
 QY 301 PNGQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPKISLVMSDAPASTTA 360
 DB 507 PNGQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPKISLVMSDAPASTTA 566
 QY 361 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDGRNNVENVFNAPOSQGTYYTIEVQAYN 420
 DB 567 SVTLVNDLDLVITAPNGTQYVGNDFTSYNDNDGRNNVENVFNAPOSQGTYYTIEVQAYN 626
 QY 421 VPVGPQTFSLAIVN 434
 DB 627 VPVGPQTFSLAIVN 640

RESULT 9
 ADM40773
 ID ADM40773 standard; protein; 640 AA.
 AC ADM40773;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Alkaline protease from Bacillus sp. KSM-KP43.
 XX
 KW alkaline protease; laundry detergent; bleaching agent; detergent;
 KW denture-cleaning agent; enzyme.
 XX
 OS Bacillus sp.; KSM-KP43.
 XX
 PN US2004072321-A1.
 XX
 PD 15-APR-2004.
 XX
 PF 09-JUN-2003; 2003US-00456479.
 XX
 PR 26-JUN-2002; 2002JP-00186387.
 PR 18-OCT-2002; 2002JP-00304232.

XX (KAOS) KAO CORP.
 XX Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
 XX WPI; 2004-328572/30.
 XX N-PSDB; ADM40772.
 XX New alkaline protease having a mutant prepro sequence where amino acid
 PT residues at positions 52, 75 and 142 are substituted with another amino
 PT acid residue, useful as enzyme component of laundry detergents, or
 PT bleaching agents.
 XX Disclosure; SEQ ID NO 4; 29pp; English.
 XX The invention relates to an alkaline protease having a prepro sequence.
 CC The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
 CC acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino
 CC acid residues at: (a) position 52 is substituted by aspartic acid or
 CC arginine; (b) position 75 is substituted by alanine or arginine; and (c)
 CC position 142 is substituted by lysine. The alkaline protease is useful as
 CC an enzyme which can be incorporated into laundry detergents, bleaching
 CC agents, detergents for cleaning hard surfaces or drainpipes, denture-
 CC cleaning agents, and detergents for sterilising medical apparatus. The
 CC present sequence represents alkaline protease from *Bacillus* sp. KSM-KP43.
 XX Sequence 640 AA;

Query Match 100.0%; Score 2247; DB 8; Length 640;
 Best Local Similarity 100.0%; Pred. No. 1.1e-158;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
 DB 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 266
 QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
 DB 267 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
 QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 327 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
 QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAQPTFTLSRSSIAPDSSF 240
 DB 387 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAQPTFTLSRSSIAPDSSF 446
 QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
 DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 506
 QY 301 PNGNOGGRVTLDKSLNVAYVNESSSLSTSOKATYSFTATAGPKPLKISLVWSDAPASTTA 360
 DB 507 PNGNOGGRVTLDKSLNVAYVNESSSLSTSOKATYSFTATAGPKPLKISLVWSDAPASTTA 566
 QY 361 SVTLVNDLVLITAPNGTQVGNDFSPYNDWMDGRNNVENVFVINAQPSGTYYIEVOAYN 420
 DB 567 SVTLVNDLVLITAPNGTQVGNDFSPYNDWMDGRNNVENVFVINAQPSGTYYIEVOAYN 626
 QY 421 VPVGPQTFLSAIVN 434
 DB 627 VPVGPQTFLSAIVN 640

RESULT 10
 ADS14437
 ID ADS14437 standard; protein; 640 AA.
 XX AC
 AC ADS14437;
 XX DT
 DT 30-DEC-2004 (first entry)
 XX

DE *Bacillus* alkaline protease KP43.
 XX protease; enzyme; alkaline protease; laundry detergent; KP43.
 XX *Bacillus* sp.; KSM-KP43.
 XX Key Location/Qualifiers
 FH Peptide 1..206
 FT Protein 207..640
 XX EPI466962-A1.
 XX 13-OCT-2004.
 XX 08-APR-2004; 2004EP-00008604.
 XX 10-APR-2003; 2003JP-00106709.
 XX (KAOS) KAO CORP.
 XX Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
 PI WPI; 2004-711313/70.
 DR N-PSDB; ADS14428.
 XX New engineered alkaline protease, useful particularly in laundry
 PT detergents, comprising specified amino acids at particular positions.
 XX Disclosure; SEQ ID NO 1; 31pp; English.
 XX The invention relates to a novel alkaline protease. The new alkaline
 CC protease comprises an amino acid sequence in which one or more amino acid
 CC residues selected from those located at 7 specific positions within
 CC ADS14427, or at positions corresponding to these positions are: position
 CC 15 (histidine), position 16 (threonine or glutamine), position 166
 CC (glycine), position 167 (valine), position 187 (serine), position 346
 CC (arginine), and position 405 (aspartic acid). The alkaline protease is
 CC useful in industry particularly in laundry detergents, but also e.g. in
 CC fibre modifying agents, leather processing agents, cosmetic compositions,
 CC bath additives, food-modifying agents, and pharmaceuticals. The present
 CC sequence represents the wild-type *Bacillus* sp. KSM-KP43 alkaline
 CC protease, KP43. The sequence is shown in the sequence listing as part of
 CC SEQ ID NO:1
 SQ Sequence 640 AA;
 Query Match 100.0%; Score 2247; DB 8; Length 640;
 Best Local Similarity 100.0%; Pred. No. 1.1e-158;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
 DB 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 266
 QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
 DB 267 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
 QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 327 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
 QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAQPTFTLSRSSIAPDSSF 240
 DB 387 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAQPTFTLSRSSIAPDSSF 446
 QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
 DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 506
 QY 301 PNGNOGGRVTLDKSLNVAYVNESSSLSTSOKATYSFTATAGPKPLKISLVWSDAPASTTA 360
 DB 507 PNGNOGGRVTLDKSLNVAYVNESSSLSTSOKATYSFTATAGPKPLKISLVWSDAPASTTA 566

Qy 361 SVTLVNDLDLVTAPNGTQYVGNDFTPYNDWGRNNVENVFVINAPOSQGTITIEVQAYN 420
 Db 567 SVTLVNDLDLVTAPNGTQYVGNDFTPYNDWGRNNVENVFVINAPOSQGTITIEVQAYN 626

Qy 421 VPVGPQTFSLAIVN 434
 Db 627 VPVGPQTFSLAIVN 640

RESULT 11
 ADT49613
 ID ADT49613 standard; protein; 641 AA.
 XX
 AC ADT49613;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE Bacillus alkaline protease.
 XX
 KW Alkaline protease; detergent; fiber modification; leather processing;
 KW cosmetic; bath additives; food-modification; pharmaceutical; enzyme.
 XX
 OS Bacillus sp. KSM-KP43.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..206
 FT Protein /note= "signal peptide"
 FT Protein 207..641
 FT Protein /note= "specifically claimed mature protein (SEQ ID 1)"
 XX
 PN EPI466970-Al.
 XX
 PD 13-OCT-2004.
 XX
 PF 08-APR-2004; 2004EP-00008605.
 XX
 PR 10-APR-2003; 2003JP-00106708.
 XX
 PA (KAOS) KAO CORP.
 PI Sato T, Okuda M, Koyama S, Izawa Y, Kobayashi T;
 XX
 DR WPI; 2004-711317/70.
 DR N-PSDB; ADT49605.
 XX
 PT New engineered alkaline protease with improved activity and thermal
 PT stability, useful particularly in detergents such as laundry detergents.
 XX
 PS Disclosure; Page 19-25; 35pp; English.
 XX
 CC The invention relates to an alkaline protease and its encoding gene. The
 CC alkaline protease can be expressed by standard recombinant methodology.
 CC The alkaline protease is useful in the industry particularly in
 CC detergents such as laundry detergents, but also in fiber modifying
 CC agents, leather processing agents, cosmetic compositions, bath additives,
 CC food-modifying agents, and pharmaceuticals. The enzyme has good activity
 CC and thermal stability. The present sequence represents an alkaline
 CC protease from Bacillus sp. KSM-KP43.
 XX
 SQ Sequence 641 AA;
 Query Match 100.0%; Score 2247; DB 8; Length 641;
 Best Local Similarity 100.0%; Pred. No. 1.1e-158;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIQVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
 Db 207 NDVARGIVKADVAQSSYGLYGQGIQVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266

Qy 61 NANDTNGHGTHTVAGSVLGNSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
 Db 267 NANDTNGHGTHTVAGSVLGNSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHTNSWGAAVNGAYTTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 Db 327 AGARIHTNSWGAAVNGAYTTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKGRIKPDVMAPOGTFILSARSSILAPDSSF 240
 Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKGRIKPDVMAPOGTFILSARSSILAPDSSF 446

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFFVKNRGITPKPSLLKAAIAGAADIGLY 300
 Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFFVKNRGITPKPSLLKAAIAGAADIGLY 506

Qy 301 PNGQGWGRVTLDKSLNVAYVNESSLSLTSQATYSFTATAGPLKISLVMSDAPASTTA 360
 Db 507 PNGQGWGRVTLDKSLNVAYVNESSLSLTSQATYSFTATAGPLKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLDLVTAPNGTQYVGNDFTPYNDWGRNNVENVFVINAPOSQGTITIEVQAYN 420
 Db 567 SVTLVNDLDLVTAPNGTQYVGNDFTPYNDWGRNNVENVFVINAPOSQGTITIEVQAYN 626

Qy 421 VPVGPQTFSLAIVN 434
 Db 627 VPVGPQTFSLAIVN 640

RESULT 12
 ADM40780
 ID ADM40780 standard; protein; 434 AA.
 XX
 AC ADM40780;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Alkaline protease #2 from Bacillus sp. KSM-KP9865.
 XX
 KW alkaline protease; laundry detergent; bleaching agent; detergent;
 KW denture-cleaning agent; enzyme.
 XX
 OS Bacillus sp.; KSM-KP9865.
 XX
 PN US2004072321-Al.
 XX
 PD 15-APR-2004.
 XX
 PF 09-JUN-2003; 2003US-00456479.
 XX
 PR 26-JUN-2002; 2002JP-00186387.
 PR 18-OCT-2002; 2002JP-00304232.
 XX
 PA (KAOS) KAO CORP.
 PI Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
 XX
 DR WPI; 2004-328572/30.
 XX
 PT New alkaline protease having a mutant prepro sequence where amino acid
 PT residues at positions 52, 75 and 142 are substituted with another amino
 PT acid residue, useful as enzyme component of laundry detergents, or
 PT bleaching agents.
 XX
 PS Disclosure; SEQ ID NO 11; 29pp; English.
 XX
 CC The invention relates to an alkaline protease having a prepro sequence.
 CC The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
 CC acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino
 CC acid residues at: (a) position 52 is substituted by aspartic acid or
 CC arginine; (b) position 75 is substituted by alanine or arginine; and (c)
 CC position 142 is substituted by lysine. The alkaline protease is useful as
 CC an enzyme which can be incorporated into laundry detergents, bleaching
 CC agents, detergents for cleaning hard surfaces or drainpipes, denture-
 CC cleaning agents, and detergents for sterilising medical apparatus. The
 CC present sequence represents an alkaline protease used in homology

CC comparison with alkaline protease from *Bacillus* sp. KSM-KP43.

XX Sequence 434 AA;
 PT Query Match 99.8%; Score 2242; DB 8; Length 434;
 PS Best Local Similarity 99.8%; Pred. No. 1.5e-158;
 SS Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAGSSVGLGSGQGVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
 Db 1 NDVARGIVKADVAGSSVGLGSGQGVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
 Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

Qy 121 AGARIHTNSGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
 Db 121 AGARIHTNSGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLPDSSF 240
 Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLPDSSF 240

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIGLY 300
 Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIGLY 300

Qy 301 PNGNQGRVTLDKSLNVAAYVNESSLSSTSQATYSFTATAGKPKLSLVWSDAPASTTA 360
 Db 301 PNGNQGRVTLDKSLNVAAYVNESSLSSTSQATYSFTATAGKPKLSLVWSDAPASTTA 360

Qy 361 SVTLVNDLDLVTAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
 Db 361 SVTLVNDLDLVTAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420

Qy 421 VPVGPQTFSLAIVN 434
 Db 421 VPVGPQTFSLAIVN 434

RESULT 13

ID ADS14441 standard; protein; 434 AA.

AC ADS14441;

XX 30-DEC-2004 (first entry)

XX *Bacillus* alkaline protease KP43 N187S mutant.

XX protease; enzyme; alkaline protease; laundry detergent; KP43; mutant;

XX muitein.

XX *Bacillus* sp.; KSM-KP43.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 187 /note= "Wild-type Asn substituted by Ser"

XX EP1466962-A1.

XX 13-OCT-2004.

XX 08-APR-2004; 2004EP-00008504.

XX 10-APR-2003; 2003JP-00106709.

XX (KAOS) KAO CORP.

XX Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;

XX Alkaline protease; *Bacillus*; casein digestion; oleic acid; enzyme;

DR WPI; 2004-711313/70.

XX New engineered alkaline protease, useful particularly in laundry
 PT detergents, comprising specified amino acids at particular positions.

XX Example 1; Page; 31pp; English.

XX The invention relates to a novel alkaline protease. The new alkaline
 CC protease comprises an amino acid sequence in which one or more amino acid
 CC residues selected from those located at 7 specific positions within
 CC ADS14427, or at positions corresponding to these positions are: position
 CC 15 (histidine), position 16 (threonine or glutamine), position 166
 CC (glycine), position 167 (valine), position 187 (serine), position 346
 CC (arginine), and position 405 (aspartic acid). The alkaline protease is
 CC useful in industry particularly in laundry detergents, but also e.g. in
 CC fibre modifying agents, leather processing agents, cosmetic compositions,
 CC bath additives, food-modifying agents, and pharmaceuticals. The present
 CC sequence represents an alkaline protease variant of the invention. Note:
 CC The present sequence is not represented in the specification, but has
 CC been created by the indexer using sequence shown in ADS14427 and
 CC information given in Example 1.

XX Sequence 434 AA;

Query Match 99.8%; Score 2242; DB 8; Length 434;

Best Local Similarity 99.8%; Pred. No. 1.5e-158;

Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAGSSVGLGSGQGVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60

Db 1 NDVARGIVKADVAGSSVGLGSGQGVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

Qy 121 AGARIHTNSGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

Db 121 AGARIHTNSGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLPDSSF 240

Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLPDSSF 240

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIGLY 300

Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIGLY 300

Qy 301 PNGNQGRVTLDKSLNVAAYVNESSLSSTSQATYSFTATAGKPKLSLVWSDAPASTTA 360

Db 301 PNGNQGRVTLDKSLNVAAYVNESSLSSTSQATYSFTATAGKPKLSLVWSDAPASTTA 360

Qy 361 SVTLVNDLDLVTAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420

Db 361 SVTLVNDLDLVTAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420

Qy 421 VPVGPQTFSLAIVN 434

Db 421 VPVGPQTFSLAIVN 434

RESULT 14

AAV17091

ID AAV17091 standard; protein; 640 AA.

XX AAV17091;

XX 20-MAR-2003 (revised)

XX 21-JUL-1999 (first entry)

XX *Bacillus* alkaline protease.

XX Alkaline protease; *Bacillus*; casein digestion; oleic acid; enzyme;

KW washing composition; oxidising agent.
 XX Bacillus sp.
 OS WO9918218-A1.
 XX 15-APR-1999.
 XX 07-OCT-1998; 98WO-JP004528.
 XX 07-OCT-1997; 97JP-00274570.
 XX (KAOS) KAO CORP.
 XX Takaiwa M, Okuda M, Saeki K, Kubota H, Hitomi J, Kageyama Y;
 FI Shikata S, Nomura M;
 XX WPI; 1999-287736/27.
 DR N-PSDB; AAX37279.
 DR Alkali protease from Bacillus used in washing powders.
 XX Disclosure; Page 63-68; 71pp; Japanese.
 XX The invention relates to alkaline proteases produced by strains of
 CC Bacillus. The proteases ability to digest casein is not inhibited by
 CC oleic acid and they have a high stability to oxidising agents. The
 CC alkaline protease of the invention has the following properties: (a) it
 CC is active over the pH range 4-13 and has at least 80% of its optimum
 CC activity over the range pH 6-12; (b) after 30 minutes at 40 deg. C it is
 CC stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d)
 CC its ability to digest casein is not inhibited by oleic acid; (e) it has
 CC molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be
 CC used as enzymes in washing compositions for use in automatic dishwashers
 CC and for washing clothes. The stability to oxidising agents allows the
 CC enzyme to be an effective component of washing compositions including
 CC bleaches. The present sequence represents an alkaline protease. (Updated
 CC on 20-MAR-2003 to correct DR field.)
 XX Sequence 640 AA;

Query Match 99.8%; Score 2242; DB 2; Length 640;
 Best Local Similarity 99.8%; Pred. No. 2.5e-158;
 Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
 DB 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 266
 QY 61 NANDTNGHGTTHVAGSVLNGSTNGKMAPOANLVFOSIMDSGGGLGGLPSNLTQLFSQAYS 120
 DB 267 NANDTNGHGTTHVAGSVLNGSTNGKMAPOANLVFOSIMDSGGGLGGLPSNLTQLFSQAYS 326
 QY 121 AGARLHTNSWGAANVGYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 327 AGARLHTNSWGAANVGYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
 QY 181 TVGATENLRPSGVSADINHVAFQSSRGPTKDGRIKPDVMAAGPTFILSARSSLAPDSF 240
 DB 387 TVGATENLRPSGVSADINHVAFQSSRGPTKDGRIKPDVMAAGPTFILSARSSLAPDSF 446
 QY 241 WANHDSKYVMGTTSMATPIVAGNVAQLREHVPKNGITPKPSLKAALIAAGADIGLY 300
 DB 447 WANHDSKYVMGTTSMATPIVAGNVAQLREHVPKNGITPKPSLKAALIAAGADIGLY 506
 QY 301 PNGNGQWGRVTLDKSLNVAYVNESSLSSTSQATYSFTATAGKPLKISLVMSDAPASTTA 360
 DB 507 PNGNGQWGRVTLDKSLNVAYVNESSLSSTSQATYSFTATAGKPLKISLVMSDAPASTTA 566
 QY 361 SVTLVNDLDLVITAPNGTQYVNDFTSPYNDWGRNNVNFVINAPOSQGTITIEVQAYN 420
 DB 567 SVTLVNDLDLVITAPNGTQYVNDFTSPYNDWGRNNVNFVINAPOSQGTITIEVQAYN 626

QY 421 VPVGQPTFSLAIVN 434
 DB 627 VPVGQPTFSLAIVN 640
 RESULT 15
 ADS14438
 ID ADS14438 standard; protein; 434 AA.
 XX ADS14438;
 AC ADS14438;
 XX 30-DEC-2004 (first entry)
 DT 30-DEC-2004 (first entry)
 DE Bacillus alkaline protease KP43 S15H/S16T mutant.
 XX protease; enzyme; alkaline protease; laundry detergent; KP43; mutant;
 KW muten.
 KW Bacillus sp.; KSM-KP43.
 OS Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 15 /note= "Wild-type Ser substituted by His"
 FT Misc-difference 16 /note= "Wild-type Ser substituted by Thr"
 FT
 FT
 FT
 XX EPI466962-A1.
 XX 13-OCT-2004.
 XX 08-APR-2004; 2004EP-00008604.
 XX 10-APR-2003; 2003JP-00106709.
 XX (KAOS) KAO CORP.
 XX Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
 XX WPI; 2004-711313/70.
 XX New engineered alkaline protease, useful particularly in laundry
 PT detergents, comprising specified amino acids at particular positions.
 XX Example 1; Page; 31pp; English.
 XX The invention relates to a novel alkaline protease. The new alkaline
 CC protease comprises an amino acid sequence in which one or more amino acid
 CC residues selected from those located at 7 specific positions within
 CC ADS14427, or at positions corresponding to these positions are: position
 CC 15 (histidine), position 16 (threonine or glutamine), position 166
 CC (glycine), position 167 (valine), position 187 (serine), position 346
 CC (arginine), and position 405 (aspartic acid). The alkaline protease is
 CC useful in industry particularly in laundry detergents, but also e.g. in
 CC fibre modifying agents, leather processing agents, cosmetic compositions,
 CC bath additives, food-modifying agents, and pharmaceuticals. The present
 CC sequence represents an alkaline protease variant of the invention. Note:
 CC The present sequence is not represented in the specification, but has
 CC been created by the indexer using sequence shown in ADS14427 and
 CC information given in Example 1.
 XX Sequence 434 AA;
 Query Match 99.6%; Score 2239; DB 8; Length 434;
 Best Local Similarity 99.5%; Pred. No. 2.5e-158;
 Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
 DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
 QY 61 NANDTNGHGTTHVAGSVLNGSTNGKMAPOANLVFOSIMDSGGGLGGLPSNLTQLFSQAYS 120

Db	61	NANDTNGHGT	HAGSVL	NGSTNKG	MAPQANL	VFQSI	MDSGG	LGGLPS	NLQTL	FSQAYS	120	
Qy	121	AGARIHTNS	GCAAVNG	AYTTDS	RNVDDY	VRKND	MTIL	FAAGNE	GPNGGT	ISAPCTAK	NAI 180	
Db	121	AGARIHTNS	GCAAVNG	AYTTDS	RNVDDY	VRKND	MTIL	FAAGNE	GPNGGT	ISAPCTAK	NAI 180	
Qy	181	TVGATENLR	PFSFGS	YADNINH	VAQFSS	RGPTK	DGR	IKPDV	MAPGT	FILSAR	SSILAPDSSF 240	
Db	181	TVGATENLR	PFSFGS	YADNINH	VAQFSS	RGPTK	DGR	IKPDV	MAPGT	FILSAR	SSILAPDSSF 240	
Qy	241	WANHDSKY	AYWGGT	SMATPI	VAGNVAQ	IREHFV	KNRGIT	PKPS	LLKAAL	IAGA	DIGLGY 300	
Db	241	WANHDSKY	AYWGGT	SMATPI	VAGNVAQ	IREHFV	KNRGIT	PKPS	LLKAAL	IAGA	DIGLGY 300	
Qy	301	PNGNOGW	GRVTL	DKSLN	VAYV	NSSSL	TSQ	KATYS	FTATAG	KPLKIS	LVMSDAPASTTA 360	
Db	301	PNGNOGW	GRVTL	DKSLN	VAYV	NSSSL	TSQ	KATYS	FTATAG	KPLKIS	LVMSDAPASTTA 360	
Qy	361	SVTLVND	LDL	VITAP	NGTQ	YVGN	DFTSP	YNDN	MDGR	NNVEN	VFINAPQSGT	YTTIEVQAYN 420
Db	361	SVTLVND	LDL	VITAP	NGTQ	YVGN	DFTSP	YNDN	MDGR	NNVEN	VFINAPQSGT	YTTIEVQAYN 420
Qy	421	VPVGPQT	FSLAIVN	434								
Db	421	VPVGPQT	FSLAIVN	434								

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